

From: Swope, Sheridan
Sent: Thursday, June 09, 2005 4:34 PM
To: STIC-Biotech/ChemLib
Subject: 10/791,980

For 10/791,980, pls search and interference search:

SID 6 against the NT and AA data bases.

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E02C70 Remsen Bld (Mailbox)

Bev Skars

6-520 ad
CB

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using bw model

Run on: June 13, 2005, 18:01:52 ; Search time 157 Seconds

(without alignments)
1269.643 Million cell updates/sec

Title: US-10-791-980-6

Perfect score: 2834

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Published Applications_AA.*
2: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
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21: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2834	100.0	520	10	US-09-862-631-6
2	2472	87.2	520	9	US-09-737-353-2
3	2472	87.2	520	9	US-09-950-510-2
4	2472	87.2	520	9	US-09-950-510-21
5	2472	87.2	520	9	US-09-950-510-24
6	2472	87.2	520	14	US-10-028-072-144
7	2472	87.2	520	14	US-10-140-808-144
8	2472	87.2	520	14	US-10-121-048-144
9	2472	87.2	520	14	US-10-123-904-144
10	2472	87.2	520	14	US-10-140-470-144
11	2472	87.2	520	14	US-10-175-746-144

12	2472	87.2	520	14	US-10-176-918-144	Sequence 144, App
13	2472	87.2	520	14	US-10-176-921-144	Sequence 144, App
14	2472	87.2	520	14	US-10-137-865-144	Sequence 144, App
15	2472	87.2	520	14	US-10-140-474-144	Sequence 144, App
16	2472	87.2	520	14	US-10-142-431-144	Sequence 144, App
17	2472	87.2	520	14	US-10-143-114-144	Sequence 144, App
18	2472	87.2	520	14	US-10-050-216B-9	Sequence 9, Appl1
19	2472	87.2	520	14	US-10-142-419-144	Sequence 144, App
20	2472	87.2	520	14	US-10-123-262-144	Sequence 144, App
21	2472	87.2	520	14	US-10-142-423-144	Sequence 144, App
22	2472	87.2	520	14	US-10-121-050-144	Sequence 144, App
23	2472	87.2	520	14	US-10-141-755-144	Sequence 144, App
24	2472	87.2	520	14	US-10-143-032-144	Sequence 144, App
25	2472	87.2	520	14	US-10-123-108-144	Sequence 144, App
26	2472	87.2	520	14	US-10-123-236-144	Sequence 144, App
27	2472	87.2	520	14	US-10-123-261-144	Sequence 144, App
28	2472	87.2	520	14	US-10-140-921-144	Sequence 144, App
29	2472	87.2	520	14	US-10-140-928-144	Sequence 144, App
30	2472	87.2	520	14	US-10-121-045-144	Sequence 144, App
31	2472	87.2	520	14	US-10-123-292-144	Sequence 144, App
32	2472	87.2	520	14	US-10-123-903-144	Sequence 144, App
33	2472	87.2	520	14	US-10-124-819-144	Sequence 144, App
34	2472	87.2	520	14	US-10-124-822-144	Sequence 144, App
35	2472	87.2	520	14	US-10-140-925-144	Sequence 144, App
36	2472	87.2	520	14	US-10-160-458-144	Sequence 144, App
37	2472	87.2	520	14	US-10-124-824-144	Sequence 144, App
38	2472	87.2	520	14	US-10-127-825A-144	Sequence 144, App
39	2472	87.2	520	14	US-10-127-829A-144	Sequence 144, App
40	2472	87.2	520	14	US-10-127-835A-144	Sequence 144, App
41	2472	87.2	520	14	US-10-127-839A-144	Sequence 144, App
42	2472	87.2	520	14	US-10-127-901A-144	Sequence 144, App
43	2472	87.2	520	14	US-10-128-633A-144	Sequence 144, App
44	2472	87.2	520	14	US-10-131-813A-144	Sequence 144, App
45	2472	87.2	520	14	US-10-131-818A-144	Sequence 144, App

ALIGNMENTS

RESULT 1
US-09-862-631-6
; Sequence 6, Application US/09862631
; Publication No. US20030032164A1
; GENERAL INFORMATION:
; APPLICANT: Holmgren, Erik
; APPLICANT: Kihlen, Mats
; APPLICANT: Wood, Tim
; APPLICANT: Ekblom, Jonas
; TITLE OF INVENTION: Novel Matrix Metalloproteinases
; FILE REFERENCE: 00014REGUS
; CURRENT APPLICATION NUMBER: US/09/862,631
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 206119
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-631-6

Query Match 100.0%; Score 2834; DB 10; Length 520;
Best local similarity 100.0%; Pred. No. 2.3e-234;
Matches 520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MWARVGLLRALQLLMGHLDAQPAERGGQELRKEAEAFLEKGYINEQVPAPTSTRS 60
DB 1 MWARVGLLRALQLLMGHLDAQPAERGGQELRKEAEAFLEKGYINEQVPAPTSTRS 60
QY 61 DAIRAFQWVSQIPVSGVLDRAFLRQMTTRPCGVDTJNSAAWAERTSDLFAHRTWMRK 120
DB 61 DAIRAFQWVSQIPVSGVLDRAFLRQMTTRPCGVDTJNSAAWAERTSDLFAHRTWMRK 120

QY 121 KRFKQGNKWKYKOHLSYRLVNMPEHLRSQFQAPCAPSSCGATSGORMSSGRPOPAPLT 180
DB 121 KRFKQGNKWKYKOHLSYRLVNMPEHLRSQFQAPCAPSSCGATSGORMSSGRPOPAPLT 180
QY 181 SCSPSSKGTITMGWAMPWAQAPWRTPTFLPRGGAHFDQDERMSLSRRGRNLFVYLAH 240
DB 181 SCSPSSKGTITMGWAMPWAQAPWRTPTFLPRGGAHFDQDERMSLSRRGRNLFVYLAH 240
QY 241 EIGHTGLTHSPAPRALMAPYKRLGRDALLSMVDVLAQSLYKGPJGGSVAVOLPKL 300
DB 241 EIGHTGLTHSPAPRALMAPYKRLGRDALLSMVDVLAQSLYKGPJGGSVAVOLPKL 300
QY 301 TDFETWDSYSPQGRREPTQGPYCHSSFDATTVDRQOOLYIFKSHFMEVAADGNVSEPR 360
DB 301 TDFETWDSYSPQGRREPTQGPYCHSSFDATTVDRQOOLYIFKSHFMEVAADGNVSEPR 360
QY 361 PLOERWVGLPNNIEAAVSLNDGDFYFFKGCRCWFRGPKRWMLPOLCAAGIPIRHDA 420
DB 361 PLOERWVGLPNNIEAAVSLNDGDFYFFKGCRCWFRGPKRWMLPOLCAAGIPIRHDA 420
QY 421 ALFPPLRLILFKGARYYVLARGGLQVEPYPRSLQDWGIGIPEEVGALPRPDGSIIF 480
DB 421 ALFPPLRLILFKGARYYVLARGGLQVEPYPRSLQDWGIGIPEEVGALPRPDGSIIF 480
QY 481 RDRYWRDLDOAKLQATTSGRWATELPMWGMCHANSALP 520
DB 481 RDRYWRDLDOAKLQATTSGRWATELPMWGMCHANSALP 520

RESULT 2

US-09-737-353-2
Sequence 2, Application US/09737353
Patent No. US20010036648A1
GENERAL INFORMATION:
APPLICANT: Christopher Donald Southan
APPLICANT: Stephen Anthony Hughes
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30222
CURRENT APPLICATION NUMBER: US/09/737,353
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: 0001898.6
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FaSTSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 520
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-737-353-2

Query Match 87.2%; Score 2472; DB 9; Length 520;
Best Local Similarity 88.9%; Pred. No. 2, 7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;
QY 1 MVARVGLLRALQILMLGHLDAQPAERGGOELRKEAEFLKXYGLNEQVPAKPTSTRFS 60
DB 1 MVARVGLLRALQILMLGHLDAQPAERGGOELRKEAEFLKXYGLNEQVPAKPTSTRFS 60
QY 61 DAIRAFQWVSQLPVSGVLDRAITLROMTRPRCGVTDNYSYAAMERISDLFARHRTKMRK 120
DB 61 DAIRAFQWVSQLPVSGVLDRAITLROMTRPRCGVTDNYSYAAMERISDLFARHRTKMRK 120
QY 121 KRFKQGNKWKYKOHLSYRLVNMPEHLRSQFQAPCAPSSCGATSG--GRWS--SGRPQ 175
DB 121 KRFKQGNKWKYKOHLSYRLVNMPEHLRSQFQAPCAPSSCGATSG--GRWS--SGRPQ 175
QY 176 QAPLTSSPSS-----KGTITMGWAMPWAQAPWRTPTFLPRGGAHFDQDERMSLSRR 229
DB 176 QAPLTSSPSS-----KGTITMGWAMPWAQAPWRTPTFLPRGGAHFDQDERMSLSRR 229
QY 229 EAPAT--GPADIRLTFQGDHNDLGNAPDGGALAAHFLPRGGAHFDQDERMSLSRR 229
DB 229 EAPAT--GPADIRLTFQGDHNDLGNAPDGGALAAHFLPRGGAHFDQDERMSLSRR 229
QY 230 RGRNLFVLAHEIGHTGLTHSPAPRALMAPYKRLGRDALLSMVDVLAQSLYKGPJG 289
DB 230 RGRNLFVLAHEIGHTGLTHSPAPRALMAPYKRLGRDALLSMVDVLAQSLYKGPJG 289

DB 230 RGRNLFVLAHEIGHTGLTHSPAPRALMAPYKRLGRDALLSMVDVLAQSLYKGPJG 289
QY 290 SVAVOLPGKLTDFETWDSYSPQGRREPTQGPYCHSSFDATTVDRQOOLYIFKSHFWE 349
DB 290 SVAVOLPGKLTDFETWDSYSPQGRREPTQGPYCHSSFDATTVDRQOOLYIFKSHFWE 349
QY 350 VAADGNVSEPRPLOERWVGLPNNIEAAVSLNDGDFYFFKGCRCWFRGPKRWMLPOLC 409
DB 350 VAADGNVSEPRPLOERWVGLPNNIEAAVSLNDGDFYFFKGCRCWFRGPKRWMLPOLC 409
QY 410 RAGGIPRHDALEFPPLRLILFKGARYYVLARGGLQVEPYPRSLQDWGIGIPEEVG 469
DB 410 RAGGIPRHDALEFPPLRLILFKGARYYVLARGGLQVEPYPRSLQDWGIGIPEEVG 469
QY 470 LPRPDGSIIFPRDWRDLDOAKLQATTSGRWATELPMWGMCHANSALP 520
DB 470 LPRPDGSIIFPRDWRDLDOAKLQATTSGRWATELPMWGMCHANSALP 520

RESULT 3

US-09-950-510-2
Sequence 2, Application US/09950510
Patent No. US20020150978A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory
TITLE OF INVENTION: 46798, A No. US20020150978A1 Human Matrix Metalloproteinase And
FILE REFERENCE: 10147-4501
CURRENT APPLICATION NUMBER: US/09/950,510
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/251,156
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 520
TYPE: PRT
ORGANISM: Homo sapiens
US-09-950-510-2

Query Match 87.2%; Score 2472; DB 9; Length 520;
Best Local Similarity 88.9%; Pred. No. 2, 7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;
QY 1 MVARVGLLRALQILMLGHLDAQPAERGGOELRKEAEFLKXYGLNEQVPAKPTSTRFS 60
DB 1 MVARVGLLRALQILMLGHLDAQPAERGGOELRKEAEFLKXYGLNEQVPAKPTSTRFS 60
QY 61 DAIRAFQWVSQLPVSGVLDRAITLROMTRPRCGVTDNYSYAAMERISDLFARHRTKMRK 120
DB 61 DAIRAFQWVSQLPVSGVLDRAITLROMTRPRCGVTDNYSYAAMERISDLFARHRTKMRK 120
QY 121 KRFKQGNKWKYKOHLSYRLVNMPEHLRSQFQAPCAPSSCGATSG--GRWS--SGRPQ 175
DB 121 KRFKQGNKWKYKOHLSYRLVNMPEHLRSQFQAPCAPSSCGATSG--GRWS--SGRPQ 175
QY 176 QAPLTSSPSS-----KGTITMGWAMPWAQAPWRTPTFLPRGGAHFDQDERMSLSRR 229
DB 176 QAPLTSSPSS-----KGTITMGWAMPWAQAPWRTPTFLPRGGAHFDQDERMSLSRR 229
QY 229 EAPAT--GPADIRLTFQGDHNDLGNAPDGGALAAHFLPRGGAHFDQDERMSLSRR 229
DB 229 EAPAT--GPADIRLTFQGDHNDLGNAPDGGALAAHFLPRGGAHFDQDERMSLSRR 229
QY 230 RGRNLFVLAHEIGHTGLTHSPAPRALMAPYKRLGRDALLSMVDVLAQSLYKGPJG 289
DB 230 RGRNLFVLAHEIGHTGLTHSPAPRALMAPYKRLGRDALLSMVDVLAQSLYKGPJG 289
QY 290 SVAVOLPGKLTDFETWDSYSPQGRREPTQGPYCHSSFDATTVDRQOOLYIFKSHFWE 349
DB 290 SVAVOLPGKLTDFETWDSYSPQGRREPTQGPYCHSSFDATTVDRQOOLYIFKSHFWE 349
QY 350 VAADGNVSEPRPLOERWVGLPNNIEAAVSLNDGDFYFFKGCRCWFRGPKRWMLPOLC 409
DB 350 VAADGNVSEPRPLOERWVGLPNNIEAAVSLNDGDFYFFKGCRCWFRGPKRWMLPOLC 409
QY 410 RAGGIPRHDALEFPPLRLILFKGARYYVLARGGLQVEPYPRSLQDWGIGIPEEVG 469
DB 410 RAGGIPRHDALEFPPLRLILFKGARYYVLARGGLQVEPYPRSLQDWGIGIPEEVG 469

Db 410 RAGGLPRHDDALFPFPLRLILFKGARYVTLARGLQVEPYPRSLQDWGIPREVSGA 469
Qy 470 LRPDGSIIFFRDDRYWRDLQAKLQATTSGRWATELPMWGCWHAHNSGSLF 520
Db 470 LRPDGSIIFFRDDRYWRDLQAKLQATTSGRWATELPMWGCWHAHNSGSLF 520

RESULT 4

US-09-950-510-21
; Sequence 21, Application US/09950510
; Patent No. US20020150978A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory
; TITLE OF INVENTION: 46798, A No. US20020150978A1el Human Matrix Metalloproteinase And
; FILE REFERENCE: 10147-45U1
; CURRENT APPLICATION NUMBER: US/09/950,510
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/251,156
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 21
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-510-21

Query Match 87.2%; Score 2472; DB 9; Length 520;
Best Local Similarity 88.9%; Pred. No. 2,7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

Qy 1 WVARVGLLRALQLLMGHLDAQPAERGGQELRKEAEAFLEKGYLNEQVPAPSTSPS 60
Db 1 WVARVGLLRALQLLMGHLDAQPAERGGQELRKEAEAFLEKGYLNEQVPAPSTSPS 60
Qy 61 DAIRAFQWVSQLPVSGVLDRAFLRQMTFRPCGVTTDNTSYAAMAEKISDLFAHRTYMRK 120
Db 61 DAIRAFQWVSQLPVSGVLDRAFLRQMTFRPCGVTTDNTSYAAMAEKISDLFAHRTYMRK 120
Qy 121 KRFPAQGNKWKYKHLSYRLVNMPEHLRSQFGAPCAPSPSSCGATS--GRSPQ 175
Db 121 KRFPAQGNKWKYKHLSYRLVNMPEHL-----PEPAVKGAVRAAFQMLSNVSLAEW 171
Qy 176 QAPLTSGSPSS-----KGTITMGWAMPPLMAQGAFWRTPELPRGSAHFDODERWSLSRR 229
Db 172 EAPAT--GPADIRLRFPGDHDNDGLGNAFDGCGALAHAFILPRGSAHFDODERWSLSRR 229
Qy 230 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALISWDVLAVQSLYKGPLG 289
Db 230 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALISWDVLAVQSLYKGPLG 289
Qy 290 SVAVOLPGKLPFDPEFTWDSYSPQGRPETQPKYCHSSFDATTVRQOOLYIFKSHFWE 349
Db 290 SVAVOLPGKLPFDPEFTWDSYSPQGRPETQPKYCHSSFDATTVRQOOLYIFKSHFWE 349
Qy 350 VAADGNVSEPRPLQGRWVGLPPIIBAAVSLNDGDFEFKGGRCWRFRPKVWGLPOLC 409
Db 350 VAADGNVSEPRPLQGRWVGLPPIIBAAVSLNDGDFEFKGGRCWRFRPKVWGLPOLC 409
Qy 410 RAGGLPRHDDALFPFPLRLILFKGARYVTLARGLQVEPYPRSLQDWGIPREVSGA 469
Db 410 RAGGLPRHDDALFPFPLRLILFKGARYVTLARGLQVEPYPRSLQDWGIPREVSGA 469
Qy 470 LRPDGSIIFFRDDRYWRDLQAKLQATTSGRWATELPMWGCWHAHNSGSLF 520
Db 470 LRPDGSIIFFRDDRYWRDLQAKLQATTSGRWATELPMWGCWHAHNSGSLF 520

RESULT 5
US-09-950-510-24
; Sequence 24, Application US/09950510
; Patent No. US20020150978A1
; GENERAL INFORMATION:

; APPLICANT: Curtis, Rory
; TITLE OF INVENTION: 46798, A No. US20020150978A1el Human Matrix Metalloproteinase And
; FILE REFERENCE: 10147-45U1
; CURRENT APPLICATION NUMBER: US/09/950,510
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/251,156
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 24
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-510-24

Query Match 87.2%; Score 2472; DB 9; Length 520;
Best Local Similarity 88.9%; Pred. No. 2,7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

Qy 1 WVARVGLLRALQLLMGHLDAQPAERGGQELRKEAEAFLEKGYLNEQVPAPSTSPS 60
Db 1 WVARVGLLRALQLLMGHLDAQPAERGGQELRKEAEAFLEKGYLNEQVPAPSTSPS 60
Qy 61 DAIRAFQWVSQLPVSGVLDRAFLRQMTFRPCGVTTDNTSYAAMAEKISDLFAHRTYMRK 120
Db 61 DAIRAFQWVSQLPVSGVLDRAFLRQMTFRPCGVTTDNTSYAAMAEKISDLFAHRTYMRK 120
Qy 121 KRFPAQGNKWKYKHLSYRLVNMPEHLRSQFGAPCAPSPSSCGATS--GRSPQ 175
Db 121 KRFPAQGNKWKYKHLSYRLVNMPEHL-----PEPAVKGAVRAAFQMLSNVSLAEW 171
Qy 176 QAPLTSGSPSS-----KGTITMGWAMPPLMAQGAFWRTPELPRGSAHFDODERWSLSRR 229
Db 172 EAPAT--GPADIRLRFPGDHDNDGLGNAFDGCGALAHAFILPRGSAHFDODERWSLSRR 229
Qy 230 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALISWDVLAVQSLYKGPLG 289
Db 230 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALISWDVLAVQSLYKGPLG 289
Qy 290 SVAVOLPGKLPFDPEFTWDSYSPQGRPETQPKYCHSSFDATTVRQOOLYIFKSHFWE 349
Db 290 SVAVOLPGKLPFDPEFTWDSYSPQGRPETQPKYCHSSFDATTVRQOOLYIFKSHFWE 349
Qy 350 VAADGNVSEPRPLQGRWVGLPPIIBAAVSLNDGDFEFKGGRCWRFRPKVWGLPOLC 409
Db 350 VAADGNVSEPRPLQGRWVGLPPIIBAAVSLNDGDFEFKGGRCWRFRPKVWGLPOLC 409
Qy 410 RAGGLPRHDDALFPFPLRLILFKGARYVTLARGLQVEPYPRSLQDWGIPREVSGA 469
Db 410 RAGGLPRHDDALFPFPLRLILFKGARYVTLARGLQVEPYPRSLQDWGIPREVSGA 469
Qy 470 LRPDGSIIFFRDDRYWRDLQAKLQATTSGRWATELPMWGCWHAHNSGSLF 520
Db 470 LRPDGSIIFFRDDRYWRDLQAKLQATTSGRWATELPMWGCWHAHNSGSLF 520

RESULT 6
US-10-028-072-144
; Sequence 144, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
FILE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/028.072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063227
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063561
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063704
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063735
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17

PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069334
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414

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/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/086430
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087106
/ PRIOR FILING DATE: 1998-05-28
/ PRIOR APPLICATION NUMBER: 60/088026
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088730
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088741
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088810
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088858
/ PRIOR FILING DATE: 1998-06-11
/ PRIOR APPLICATION NUMBER: 60/089532
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089599
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089907
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/089947
/ PRIOR FILING DATE: 1998-06-19
/ PRIOR APPLICATION NUMBER: 60/090349
/ PRIOR FILING DATE: 1998-06-23
/ PRIOR APPLICATION NUMBER: 60/090429
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090445
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090538
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090663
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: 60/091360
/ PRIOR FILING DATE: 1998-07-01
/ PRIOR APPLICATION NUMBER: 60/091519
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091982
/ PRIOR FILING DATE: 1998-07-07
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Query Match      87.2%; Score 2472; DB 14; Length 520;
Best Local Similarity 88.9%; Pred. No. 2.7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MVARVGLLRALQLLLMGLHDAOPARGGQELRKEAEFLKXGYLNEQVPAPTSTRS 60
DB 1 MVARVGLLRALQLLLMGLHDAOPARGGQELRKEAEFLKXGYLNEQVPAPTSTRS 60
QY 61 DAIRAFQWVSQLPVSGVLDRAITLROMTRPRCGVTDNTSYAAMAEISDLFAHRTQMRK 120
DB 61 DAIRAFQWVSQLPVSGVLDRAITLROMTRPRCGVTDNTSYAAMAEISDLFAHRTQMRK 120
QY 121 KRPAKGNKMYKQHLSTYRLVNPBEHLRSQFAPCAPSSCGATS--GRWS--SGRPOP 175
DB 121 KRPAKGNKMYKQHLSTYRLVNPBEHLRSQFAPCAPSSCGATS--GRWS--SGRPOP 175
QY 176 QAPLTSGPS-----KGTTMGAMPLMAOGAPMRTPLPRRGAHFDDERWSLSR 229
DB 176 QAPLTSGPS-----KGTTMGAMPLMAOGAPMRTPLPRRGAHFDDERWSLSR 229
QY 230 RGRNLFVYLAHEIGTGLTHSPAPRALMAPYKRLGRDALLSMDVLAQSLYKGPLG 289
DB 230 RGRNLFVYLAHEIGTGLTHSPAPRALMAPYKRLGRDALLSMDVLAQSLYKGPLG 289
QY 290 SVAVOLPGKLFDTFETWDSYSPQGRPETQGRPKYCHSSFDALITVDROOOLYFKGSHFWE 349
DB 290 SVAVOLPGKLFDTFETWDSYSPQGRPETQGRPKYCHSSFDALITVDROOOLYFKGSHFWE 349
QY 350 VAADGNVSEPRPLQERWGLPNIEAAAVSLNDGDPYFPKGRGCMFRGPKVWGLPOLC 409
DB 350 VAADGNVSEPRPLQERWGLPNIEAAAVSLNDGDPYFPKGRGCMFRGPKVWGLPOLC 409
QY 410 RAGGLPRHDDALFFPPLRLILFKGARYYVLARGGLOVEPYPRSLDOWGIPREVSQA 469
```

```
DB 410 RAGGLPRHDDALFFPPLRLILFKGARYYVLARGGLOVEPYPRSLDOWGIPREVSQA 469
QY 470 LRPDGSIIFFRDDRWRMDQAKLQATTSGRATELPMWGCYHANSGLALF 520
DB 470 LRPDGSIIFFRDDRWRMDQAKLQATTSGRATELPMWGCYHANSGLALF 520
```

RESULT 7

```
US-10-140-808-144
/ Sequence 144, Application US/10140808
/ Publication No. US20030017563A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Bergsini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3310R1C182
/ CURRENT APPLICATION NUMBER: US/10/140,808
/ CURRENT FILING DATE: 2002-05-07
/ Prior Application removed - See file Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 144
/ LENGTH: 520
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-140-808-144
```

```
Query Match      87.2%; Score 2472; DB 14; Length 520;
Best Local Similarity 88.9%; Pred. No. 2.7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MVARVGLLRALQLLLMGLHDAOPARGGQELRKEAEFLKXGYLNEQVPAPTSTRS 60
DB 1 MVARVGLLRALQLLLMGLHDAOPARGGQELRKEAEFLKXGYLNEQVPAPTSTRS 60
QY 61 DAIRAFQWVSQLPVSGVLDRAITLROMTRPRCGVTDNTSYAAMAEISDLFAHRTQMRK 120
DB 61 DAIRAFQWVSQLPVSGVLDRAITLROMTRPRCGVTDNTSYAAMAEISDLFAHRTQMRK 120
QY 121 KRPAKGNKMYKQHLSTYRLVNPBEHLRSQFAPCAPSSCGATS--GRWS--SGRPOP 175
DB 121 KRPAKGNKMYKQHLSTYRLVNPBEHLRSQFAPCAPSSCGATS--GRWS--SGRPOP 175
QY 176 QAPLTSGPS-----KGTTMGAMPLMAOGAPMRTPLPRRGAHFDDERWSLSR 229
DB 176 QAPLTSGPS-----KGTTMGAMPLMAOGAPMRTPLPRRGAHFDDERWSLSR 229
QY 230 RGRNLFVYLAHEIGTGLTHSPAPRALMAPYKRLGRDALLSMDVLAQSLYKGPLG 289
DB 230 RGRNLFVYLAHEIGTGLTHSPAPRALMAPYKRLGRDALLSMDVLAQSLYKGPLG 289
QY 290 SVAVOLPGKLFDTFETWDSYSPQGRPETQGRPKYCHSSFDALITVDROOOLYFKGSHFWE 349
DB 290 SVAVOLPGKLFDTFETWDSYSPQGRPETQGRPKYCHSSFDALITVDROOOLYFKGSHFWE 349
QY 350 VAADGNVSEPRPLQERWGLPNIEAAAVSLNDGDPYFPKGRGCMFRGPKVWGLPOLC 409
```

Db 350 VAADGVSEBPRLOERWGLPNIIEAAVSLNDGDFYFFKGGRCWRFRGPKVWGLPOLC 409
Qy 410 RAGGLPRHPDALFFPPLRLILFKGARYYVLARGLQVEBPYPSLQDWGCIPEEVSQA 469
Db 410 RAGGLPRHPDALFFPPLRLILFKGARYYVLARGLQVEBPYPSLQDWGCIPEEVSQA 469
Qy 470 LPRPDGSIIFPRDRYWRDLQAKLQATTSGRWATELPMWGCWANHSGSALF 520
Db 470 LPRPDGSIIFPRDRYWRDLQAKLQATTSGRWATELPMWGCWANHSGSALF 520

RESULT 8

US-10-121-049-144
Sequence 144, Application US/10121049
Publication No. US2003002239A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Geo, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C17
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 144
LENGTH: 520
TYPE: PRT
ORGANISM: Homo Sapien
US-10-121-049-144

Query Match 87.2%; Score 2472; DB 14; Length 520;
Best Local Similarity 88.9%; Pred. No. 2,7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

Qy 1 MVARVGLLLRALQLLMGLHDQAPERGGQELRKEAEFLKXGYLNEQVPAPTSTRFS 60
Db 1 MVARVGLLLRALQLLMGLHDQAPERGGQELRKEAEFLKXGYLNEQVPAPTSTRFS 60
Qy 61 DAIRAFQWVSQLPVSGVLDRAITLRQMTFRPGCVTDJNSYAAAEIRISDLFAHRTTKMRK 120
Db 61 DAIRAFQWVSQLPVSGVLDRAITLRQMTFRPGCVTDJNSYAAAEIRISDLFAHRTTKMRK 120
Qy 121 KRPAQGNKWKYKQHLSTYRLVWVPEHLRSROFAPCAPSSCGATS---QRMS--SGRPOP 175
Db 121 KRPAQGNKWKYKQHLSTYRLVWVPEHLRSROFAPCAPSSCGATS---QRMS--SGRPOP 175
Qy 176 QAPLTSGSPSS-----KGTITMGWAMPMLMAQAPMRTPLPRRGEAHFDDERWSLSRR 229
Db 172 EAPAT--GPADIRLTFFQGDHNDGIGNAFDGPGLAAHAFPRRGEAHFDDERWSLSRR 229
Qy 230 RGRNLFVVLAAHEIGTTLGLTHSPAPRALMAPIYKRLGRDALISWDVTLAVOSLYGKPLGG 289
Db 230 RGRNLFVVLAAHEIGTTLGLTHSPAPRALMAPIYKRLGRDALISWDVTLAVOSLYGKPLGG 289
Qy 290 SVAVQLPGLKFTDPETWDSYSPQGRBPETQGPYKCHSSPFAITVVDKQQLYTFKSGHFW 349
Db 290 SVAVQLPGLKFTDPETWDSYSPQGRBPETQGPYKCHSSPFAITVVDKQQLYTFKSGHFW 349

Qy 350 VAADGVSEBPRLOERWGLPNIIEAAVSLNDGDFYFFKGGRCWRFRGPKVWGLPOLC 409
Db 350 VAADGVSEBPRLOERWGLPNIIEAAVSLNDGDFYFFKGGRCWRFRGPKVWGLPOLC 409
Qy 410 RAGGLPRHPDALFFPPLRLILFKGARYYVLARGLQVEBPYPSLQDWGCIPEEVSQA 469
Db 410 RAGGLPRHPDALFFPPLRLILFKGARYYVLARGLQVEBPYPSLQDWGCIPEEVSQA 469
Qy 470 LPRPDGSIIFPRDRYWRDLQAKLQATTSGRWATELPMWGCWANHSGSALF 520
Db 470 LPRPDGSIIFPRDRYWRDLQAKLQATTSGRWATELPMWGCWANHSGSALF 520

RESULT 9

US-10-123-904-144
Sequence 144, Application US/10123904
Publication No. US2003002238A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Geo, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C54
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 144
LENGTH: 520
TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-904-144

Query Match 87.2%; Score 2472; DB 14; Length 520;
Best Local Similarity 88.9%; Pred. No. 2,7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

Qy 1 MVARVGLLLRALQLLMGLHDQAPERGGQELRKEAEFLKXGYLNEQVPAPTSTRFS 60
Db 1 MVARVGLLLRALQLLMGLHDQAPERGGQELRKEAEFLKXGYLNEQVPAPTSTRFS 60
Qy 61 DAIRAFQWVSQLPVSGVLDRAITLRQMTFRPGCVTDJNSYAAAEIRISDLFAHRTTKMRK 120
Db 61 DAIRAFQWVSQLPVSGVLDRAITLRQMTFRPGCVTDJNSYAAAEIRISDLFAHRTTKMRK 120
Qy 121 KRPAQGNKWKYKQHLSTYRLVWVPEHLRSROFAPCAPSSCGATS---QRMS--SGRPOP 175
Db 121 KRPAQGNKWKYKQHLSTYRLVWVPEHLRSROFAPCAPSSCGATS---QRMS--SGRPOP 175
Qy 176 QAPLTSGSPSS-----KGTITMGWAMPMLMAQAPMRTPLPRRGEAHFDDERWSLSRR 229
Db 172 EAPAT--GPADIRLTFFQGDHNDGIGNAFDGPGLAAHAFPRRGEAHFDDERWSLSRR 229
Qy 230 RGRNLFVVLAAHEIGTTLGLTHSPAPRALMAPIYKRLGRDALISWDVTLAVOSLYGKPLGG 289
Db 230 RGRNLFVVLAAHEIGTTLGLTHSPAPRALMAPIYKRLGRDALISWDVTLAVOSLYGKPLGG 289

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QY 290 SVAVOLPGKLTFTDFETWDSYSPQGRRPETQGRKYCHSSFDATITVDRQOOLYIFKSGHFW 349
DB 290 SVAVOLPGKLTFTDFETWDSYSPQGRRPETQGRKYCHSSFDATITVDRQOOLYIFKSGHFW 349
QY 350 VAADGVNSRPRLQGRWVGLPPIEAAVSLNDGDFYFFKGRGRCWRFRGPKYVWGLPQLC 409
DB 350 VAADGVNSRPRLQGRWVGLPPIEAAVSLNDGDFYFFKGRGRCWRFRGPKYVWGLPQLC 409
QY 410 RAGGLPRHDDALFFPRLRLILFKGARYYVLARGLQVEPYRPSLDWMGIPREVSGA 469
DB 410 RAGGLPRHDDALFFPRLRLILFKGARYYVLARGLQVEPYRPSLDWMGIPREVSGA 469
QY 470 LRPDGSIIFFRDDRWRDLQAKLQATTSGRWATELPMWGMHANSGLALF 520
DB 470 LRPDGSIIFFRDDRWRDLQAKLQATTSGRWATELPMWGMHANSGLALF 520

RESULT 10
US-10-140-470-144
; Sequence 144, Application US/10140470
; Publication No. US2003002231A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 144
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-144

Query Match 87.2%; Score 2472; DB 14; Length 520;
Best Local Similarity 88.9%; Pred. No. 2,7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;
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DB 230 RGRNLFVVLAAHIGTILGLTHSPAPRALMAPYKRLGRDALLSWDVLAVQSLYXGKPLGG 289
QY 290 SVAVOLPGKLTFTDFETWDSYSPQGRRPETQGRKYCHSSFDATITVDRQOOLYIFKSGHFW 349
DB 290 SVAVOLPGKLTFTDFETWDSYSPQGRRPETQGRKYCHSSFDATITVDRQOOLYIFKSGHFW 349
QY 350 VAADGVNSRPRLQGRWVGLPPIEAAVSLNDGDFYFFKGRGRCWRFRGPKYVWGLPQLC 409
DB 350 VAADGVNSRPRLQGRWVGLPPIEAAVSLNDGDFYFFKGRGRCWRFRGPKYVWGLPQLC 409
QY 410 RAGGLPRHDDALFFPRLRLILFKGARYYVLARGLQVEPYRPSLDWMGIPREVSGA 469
DB 410 RAGGLPRHDDALFFPRLRLILFKGARYYVLARGLQVEPYRPSLDWMGIPREVSGA 469
QY 470 LRPDGSIIFFRDDRWRDLQAKLQATTSGRWATELPMWGMHANSGLALF 520
DB 470 LRPDGSIIFFRDDRWRDLQAKLQATTSGRWATELPMWGMHANSGLALF 520

RESULT 11
US-10-175-746-144
; Sequence 144, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 144
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-144

Query Match 87.2%; Score 2472; DB 14; Length 520;
Best Local Similarity 88.9%; Pred. No. 2,7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;
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Db 172 EAPAT--GPADIRLTFQGDHNDIGLGNAPDGGALAHAFLLPRRGEAHFPDDERMSLSRR 229
QY 230 RGRNLFVYLAHEIGHTLGLTHTSPAPRALMAPYKRLGSDALLSMDVLAVOSLYGKPLGG 289
Db 230 RGRNLFVYLAHEIGHTLGLTHTSPAPRALMAPYKRLGSDALLSMDVLAVOSLYGKPLGG 289
QY 290 SVAVOLPEKLTFTDEFTWDSYSPQGRRPETQPKYCHSFDALITVDROOQLYIFKGSHPWE 349
Db 290 SVAVOLPEKLTFTDEFTWDSYSPQGRRPETQPKYCHSFDALITVDROOQLYIFKGSHPWE 349
QY 350 VAAOVNSEPRPLQERWVGLPPNIEAAVSLNDGDFYFFKGCRCMRFRGPVWGLPOLC 409
Db 350 VAAOVNSEPRPLQERWVGLPPNIEAAVSLNDGDFYFFKGCRCMRFRGPVWGLPOLC 409
QY 410 RAGGLPRHPDAALEFPPLRLILFKGARYYVLARGLQVEPYPRSLQDWGCIPEEVSQA 469
Db 410 RAGGLPRHPDAALEFPPLRLILFKGARYYVLARGLQVEPYPRSLQDWGCIPEEVSQA 469
QY 470 LPRPDGSIIFPRDDRWRDLQAKLQATTSGRWATELPMWGMHANSGLALF 520
Db 470 LPRPDGSIIFPRDDRWRDLQAKLQATTSGRWATELPMWGMHANSGLALF 520

RESULT 12
US-10-176-918-144
; Sequence 144, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 144
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-144

Query Match 87.2%; Score 2472; DB 14; Length 520;
Best Local Similarity 88.9%; Pred. No. 2.7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;
QY 1 MVARVGLLRALQLLWGHLDAPARGGQELRKEAEFLFKYGLNEQVPAKPTSTRS 60
Db 1 MVARVGLLRALQLLWGHLDAPARGGQELRKEAEFLFKYGLNEQVPAKPTSTRS 60
QY 61 DAIRAFQWVSQLPVSGVLDRAITLQMTTRPCGVTDITNSYAAMABRISDLFARHRTKMRK 120
Db 61 DAIRAFQWVSQLPVSGVLDRAITLQMTTRPCGVTDITNSYAAMABRISDLFARHRTKMRK 120
QY 121 KRFAQGNKMYKQHLSTRLVNWPEHLASRQFGAPCAPSSCGATS---QRMS--SRPOP 175
Db 121 KRFAQGNKMYKQHLSTRLVNWPEHLASRQFGAPCAPSSCGATS---QRMS--SRPOP 175

QY 176 QAPLTSGPS--KQTTMGWAMPLMQAGAWRTPLPRRGEAHFPDDERMSLSRR 229
Db 172 EAPAT--GPADIRLTFQGDHNDIGLGNAPDGGALAHAFLLPRRGEAHFPDDERMSLSRR 229
QY 230 RGRNLFVYLAHEIGHTLGLTHTSPAPRALMAPYKRLGSDALLSMDVLAVOSLYGKPLGG 289
Db 230 RGRNLFVYLAHEIGHTLGLTHTSPAPRALMAPYKRLGSDALLSMDVLAVOSLYGKPLGG 289
QY 290 SVAVOLPEKLTFTDEFTWDSYSPQGRRPETQPKYCHSFDALITVDROOQLYIFKGSHPWE 349
Db 290 SVAVOLPEKLTFTDEFTWDSYSPQGRRPETQPKYCHSFDALITVDROOQLYIFKGSHPWE 349
QY 350 VAAOVNSEPRPLQERWVGLPPNIEAAVSLNDGDFYFFKGCRCMRFRGPVWGLPOLC 409
Db 350 VAAOVNSEPRPLQERWVGLPPNIEAAVSLNDGDFYFFKGCRCMRFRGPVWGLPOLC 409
QY 410 RAGGLPRHPDAALEFPPLRLILFKGARYYVLARGLQVEPYPRSLQDWGCIPEEVSQA 469
Db 410 RAGGLPRHPDAALEFPPLRLILFKGARYYVLARGLQVEPYPRSLQDWGCIPEEVSQA 469
QY 470 LPRPDGSIIFPRDDRWRDLQAKLQATTSGRWATELPMWGMHANSGLALF 520
Db 470 LPRPDGSIIFPRDDRWRDLQAKLQATTSGRWATELPMWGMHANSGLALF 520

RESULT 13
US-10-176-921-144
; Sequence 144, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C286
; CURRENT APPLICATION NUMBER: US/10/176,921
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 144
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-921-144

Query Match 87.2%; Score 2472; DB 14; Length 520;
Best Local Similarity 88.9%; Pred. No. 2.7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;
QY 1 MVARVGLLRALQLLWGHLDAPARGGQELRKEAEFLFKYGLNEQVPAKPTSTRS 60
Db 1 MVARVGLLRALQLLWGHLDAPARGGQELRKEAEFLFKYGLNEQVPAKPTSTRS 60
QY 61 DAIRAFQWVSQLPVSGVLDRAITLQMTTRPCGVTDITNSYAAMABRISDLFARHRTKMRK 120
Db 61 DAIRAFQWVSQLPVSGVLDRAITLQMTTRPCGVTDITNSYAAMABRISDLFARHRTKMRK 120

QY 121 KRFAKQKKWKYKQHLSTYLVNMPHLSRROFGAPCAPSSCGATS---ORMS--SGRPOP 175
DB 121 KRFAKQKKWKYKQHLSTYLVNMPHLSRROFGAPCAPSSCGATS---ORMS--SGRPOP 175
QY 176 QAPLTSSGSPSS-----KGTMTGWAMPMLMOGAPWRTPEFLPRRGEAHFDODERMSLSR 229
DB 172 EAPAT--GPADIRLTFPGQDNHNDGLGNAPDGGALAHAFPRRGEAHFDODERMSLSR 229
QY 220 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKXKLGSDALISMDVLAVOGLYKXPLCG 289
DB 220 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKXKLGSDALISMDVLAVOGLYKXPLCG 289
QY 290 SVAVOLPGKLTFTDFETWDSYSPQGRRPETQGPYCHSSFDATTVDRQOOLYFKXSHFWE 349
DB 290 SVAVOLPGKLTFTDFETWDSYSPQGRRPETQGPYCHSSFDATTVDRQOOLYFKXSHFWE 349
QY 350 VAADGNVSEPRPLOGRWGLPNNIEAAVSLNDGDFYFFKGGRCWRFRGPKVWGLPOLC 409
DB 350 VAADGNVSEPRPLOGRWGLPNNIEAAVSLNDGDFYFFKGGRCWRFRGPKVWGLPOLC 409
QY 410 RAGGLPRHPDALLFPPLRLILFKGARYVYLARGILOVEPYPSLODMGSIPEVSGA 469
DB 410 RAGGLPRHPDALLFPPLRLILFKGARYVYLARGILOVEPYPSLODMGSIPEVSGA 469
QY 470 LPRPDGSIIFPRDDRYWRLDQAKLQATTSGRWATELPMWGCWANHSGSALF 520
DB 470 LPRPDGSIIFPRDDRYWRLDQAKLQATTSGRWATELPMWGCWANHSGSALF 520

RESULT 14
US-10-137-865-144
Sequence 144, Application US/10137865
Publication No. US20030032155A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunes, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C154
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 144
LENGTH: 520
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-865-144

Query Match 87.2%; Score 2472; DB 14; Length 520;
Best Local Similarity 88.9%; Pred. No. 2,7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MVARVGLLRALQLLWGLHLDQAPARGOELRKEAEAFLEKYGYLVNQPAPPTSTPS 60
DB 1 MVARVGLLRALQLLWGLHLDQAPARGOELRKEAEAFLEKYGYLVNQPAPPTSTPS 60
QY 61 DAIRAFQWVSQLPVSGVLDRAITLRQMTPRRCGVDTNTSYAAMERISDLFAHRTKMRK 120

DB 61 DAIRAFQWVSQLPVSGVLDRAITLRQMTPRRCGVDTNTSYAAMERISDLFAHRTKMRK 120
QY 121 KRFAKQKKWKYKQHLSTYLVNMPHLSRROFGAPCAPSSCGATS---ORMS--SGRPOP 175
DB 121 KRFAKQKKWKYKQHLSTYLVNMPHLSRROFGAPCAPSSCGATS---ORMS--SGRPOP 175
QY 176 QAPLTSSGSPSS-----KGTMTGWAMPMLMOGAPWRTPEFLPRRGEAHFDODERMSLSR 229
DB 172 EAPAT--GPADIRLTFPGQDNHNDGLGNAPDGGALAHAFPRRGEAHFDODERMSLSR 229
QY 220 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKXKLGSDALISMDVLAVOGLYKXPLCG 289
DB 220 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKXKLGSDALISMDVLAVOGLYKXPLCG 289
QY 290 SVAVOLPGKLTFTDFETWDSYSPQGRRPETQGPYCHSSFDATTVDRQOOLYFKXSHFWE 349
DB 290 SVAVOLPGKLTFTDFETWDSYSPQGRRPETQGPYCHSSFDATTVDRQOOLYFKXSHFWE 349
QY 350 VAADGNVSEPRPLOGRWGLPNNIEAAVSLNDGDFYFFKGGRCWRFRGPKVWGLPOLC 409
DB 350 VAADGNVSEPRPLOGRWGLPNNIEAAVSLNDGDFYFFKGGRCWRFRGPKVWGLPOLC 409
QY 410 RAGGLPRHPDALLFPPLRLILFKGARYVYLARGILOVEPYPSLODMGSIPEVSGA 469
DB 410 RAGGLPRHPDALLFPPLRLILFKGARYVYLARGILOVEPYPSLODMGSIPEVSGA 469
QY 470 LPRPDGSIIFPRDDRYWRLDQAKLQATTSGRWATELPMWGCWANHSGSALF 520
DB 470 LPRPDGSIIFPRDDRYWRLDQAKLQATTSGRWATELPMWGCWANHSGSALF 520

RESULT 15
US-10-140-474-144
Sequence 144, Application US/10140474
Publication No. US20030032156A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunes, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C162
CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 144
LENGTH: 520
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-474-144

Query Match 87.2%; Score 2472; DB 14; Length 520;
Best Local Similarity 88.9%; Pred. No. 2,7e-203;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MVARVGLLRALQLLWGLHLDQAPARGOELRKEAEAFLEKYGYLVNQPAPPTSTPS 60
DB 1 MVARVGLLRALQLLWGLHLDQAPARGOELRKEAEAFLEKYGYLVNQPAPPTSTPS 60

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Db      1  MVAHVGLLRALQILLWGHLDADPAERGGELRKEAEFLKYGYLENVQVPAKPTSTRPS 60
Qy      61  DAIRAFQWVSQLPVSGVLDRAATLRQMTPRCGVDTNVSYAAMAEISDLFARHRTKMRK 120
Db      61  DAIRAFQWVSQLPVSGVLDRAATLRQMTPRCGVDTNVSYAAMAEISDLFARHRTKMRK 120
Qy      121  KRFAKQGNKMYKQHLSTRLVNWPBHLRSROFGAPCAPSSCGATS--QRWS--SGRPOP 175
Db      121  KRFAKQGNKMYKQHLSTRLVNWPBHL-----PEPAVRGAVRAAFQIMSNVSALEFW 171
Qy      176  QABLTSGSPSS-----KGTITGMWMPLMAOGAPWRTPELPRGSAHFDDDERWLSRR 229
Db      172  EADAT--GPADILRTFFQGDHNDGLGNAFPDGGALAHAFLEPRGSAHFDDDERWLSRR 229
Qy      230  RGRNLFVYVLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALSWDDVLAQSLYGKPLGG 289
Db      230  RGRNLFVYVLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALSWDDVLAQSLYGKPLGG 289
Qy      290  SVAVOLPGKLFETWDSVSPQGRPEYQPKYCHSSFDATTVDRQOOLYTFKSHFWE 349
Db      290  SVAVOLPGKLFETWDSVSPQGRPEYQPKYCHSSFDATTVDRQOOLYTFKSHFWE 349
Qy      350  VAADGNVSEBRPLQERWVGLPVIEAAVSLNDGDFYFFKGGRCWRFRGPKFVWGLPOLC 409
Db      350  VAADGNVSEBRPLQERWVGLPVIEAAVSLNDGDFYFFKGGRCWRFRGPKFVWGLPOLC 409
Qy      410  RAGGLPRHPDALFFPPLRLILFKGARYYVLARGGLOVEPYPRSLQDWGIPREVSGA 469
Db      410  RAGGLPRHPDALFFPPLRLILFKGARYYVLARGGLOVEPYPRSLQDWGIPREVSGA 469
Qy      470  LPRPDGSIIFRRDDRYRLDOAKLOATTSGRWATELPMWGCWHANSGSALP 520
Db      470  LPRPDGSIIFRRDDRYRLDOAKLOATTSGRWATELPMWGCWHANSGSALP 520
```

Search completed: June 13, 2005, 18:15:10
Job time : 159 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using bw model

Run on: June 13, 2005, 17:24:41 ; Search time 42 seconds
(without alignments)
1191.255 Million cell updates/sec

Title: US-10-791-980-6
Perfect score: 2834
Sequence: 1 MVARVGLLRALLQLLWGHLL.....WATELPMWGMWANSGLALP 520

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	546	19.3	508	2 JCS082	matrix metalloprot
2	534	18.3	669	2 I38029	matrix metalloprot
3	517.5	18.3	582	2 I64471	matrix metalloprot
4	514.5	18.2	582	2 I38028	matrix metalloprot
5	466.5	16.5	492	2 A44399	stromelysin 3 (EC
6	463.5	16.4	582	2 I48673	matrix metalloprot
7	463	16.3	491	2 JG6197	stromelysin 3 (EC
8	455.5	16.1	488	2 S33423	stromelysin 3 (EC
9	448.5	15.8	477	1 KCHUS1	stromelysin 1 (EC
10	427	15.1	475	1 KCHTIR	stromelysin 1 (EC
11	426.5	15.0	471	1 A53711	collagenase 3 (EC
12	425.5	15.0	476	1 KCHT52	stromelysin 2 (EC
13	410	14.5	483	2 JCS743	matrix metalloprot
14	407.5	14.4	466	2 A23685	interstitial colla
15	406	14.3	476	1 UC6505	stromelysin 2 (EC
16	398	14.1	469	1 KCHU1	interstitial colla
17	398	14.0	477	1 KCHUS1	stromelysin 1 (EC
18	392	13.8	476	1 KCHUS2	stromelysin 2 (EC
19	391.5	13.8	470	2 A49499	metalloelastase HM
20	391	13.8	478	1 KCHBS1	stromelysin 1 (EC
21	388.5	13.7	472	2 S29243	interstitial colla
22	386	13.6	468	1 KCHBI	interstitial colla
23	378	13.3	477	1 I51645	stromelysin 3 (EC
24	368.5	13.0	469	1 KCPGI	interstitial colla
25	366	12.9	462	2 A42401	macrophage elastas
26	355.5	12.5	587	2 S41409	envelysin (EC 3.4.
27	353.5	12.5	587	2 S12805	envelysin (EC 3.4.
28	345.5	12.2	663	1 S46492	gelatinase A (EC 3
29	344.5	12.2	467	1 KCHUN	neutrophil collage

30	340.5	12.0	469	1 KCB01	interstitial colla
31	336.5	11.9	662	2 S70365	gelatinase A (EC 3
32	323.5	11.4	660	3 A28153	gelatinase A (EC 3
33	322	11.4	662	2 S34780	gelatinase A (EC 3
34	318.5	11.2	712	1 I46031	gelatinase B (EC 3
35	316.5	11.2	707	1 A53796	gelatinase B (EC 3
36	313	11.0	662	2 A42496	gelatinase A (EC 3
37	307	10.8	730	1 I52580	gelatinase B (EC 3
38	307	10.8	730	2 JG1456	gelatinase B (EC 3
39	303.5	10.7	616	2 JG7776	matrix metalloprot
40	301.5	10.6	707	1 A24458	gelatinase B (EC 3
41	293	10.3	708	2 UC4364	gelatinase B (EC 3
42	291.5	10.3	579	2 T37248	probable matrix me
43	291.5	10.3	598	2 T32166	hypothetical prote
44	278	9.8	521	2 T37252	probable matrix me
45	278	9.8	708	2 S62907	gelatinase B (EC 3

ALIGNMENTS

RESULT 1

JCS082
matrix metalloproteinase 18 (EC 3.4.24.-) precursor - human
C.Species: Homo sapiens (man)
C.Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C.Accession: JCS082
R.Cosine, J., Dudgeon, T.J., Catlin, G., Gearing, A.J.H., Clements, J.M.
Biochem. Biophys. Res. Commun. 228, 494-498, 1996
A.Title: Identification of MMP-18, a putative novel human matrix metalloproteinase.
A.Reference number: JCS082; MUID:97079209; PMID:8920941
A.Accession: JCS082
A.Statut: nucleic acid sequence not shown
A.Molecule type: mRNA
A.Residues: 1-508 <COS>
A.Cross-references: UNIPROT:Q99542; GB:Y08622
A.Comment: This enzyme is involved in organ morphogenesis, embryonic development and pat
tion and metastasis.
C.Genetics:
A.Gene: GDB:16MP18
A.Cross-references: GDB:5584569; OMIM:601807
C.Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C.Keywords: hydrolase; metalloproteinase; zinc; zymogen
F.1-18/Domain: signal sequence #status predicted <SIG>
F.53-256/Domain: matrix metalloproteinase homology <MMP>
F.283-472/Domain: hemopexin repeat homology <PNX>
F.185,212,216,222/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F.212,216,222/Binding site: zinc, catalytic (His) (active) #status predicted
F.213/Active site: Glu #status predicted

Query Match	19.3%	Score 546	DB 2	Length 508	
Best Local Similarity	31.4%	Pred. No. 1.5e-33			
Matches	158	Conservative 75	Mismatches 178	Indels 92	Gaps 19
QY	39	FLKRYGLNEQVPAAPTSTRF-----	SDAIRAFQWVSQLPVSGVLDRLATLQMTFRPGCV	93	
	:	:	:	:	:
DB	31	YLSQYGLQKPL-----	BGSNNFKPEDITFALRAFQEASLTPVSGQDDATRARMPQRCGL	87	
QY	94	TDYMSYAAMERISDLFARHRTKRRKRRKQGNKTKQHLSTRLVNMPHLASRQGA	153		
	:	:	:	:	:
DB	88	EDFPN-----	OKTLKYLILG-RMRKKILTRILNLPSTL-----	120	
QY	154	PCAPSSGCA-----	TSQKSSGRRPOQAPLT-----	194	
	:	:	:	:	:
DB	121	---PPTIRALRLRAFQDMN-----	VAPLTFQVQAGADIRLSFGRQSSYCSNTFDG	172	
QY	195	AMPLMAQAPWRTPPLPRGSAHFDQDERWLSRRGRNLPVLAHEIGTLGLTHSPAP	254		
	:	:	:	:	:
DB	173	PGRVLAHND-----	IPELGSHVHDEDEFTGTYRGVNLRIIAAHEVGHALGSHSYSS	226	
QY	255	RALMAFYTKRGRALLSMQDVLAQSYKGRPLGSGVAVVQPLGKLTDFEWDSDSPQR	314		
	:	:	:	:	:
DB	227	QALMAFVGEYRPHFKLHPDDVAGIQALYGKK-----	SPVIRDEBBEETELPT---VPPVPT	280	

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0Y 315 RETGQPKXCHSFDAITVDROOQLIFKSGHFWELALGONSEPPFL---QERNVGLPP 371
Db 281 EESPMPDPCSCSELDDMMGLPRGKTAFAFGDYVMVSDSG---PPGLPRVALMEGLPG 335
0Y 372 NIEAAVSLINDDPFFFKGRCMRFRGPKPPWGLPOLCAGGLPHRDPALBPPPLRLI 431
Db 336 NLDAVSPRTQWIHFFKGDKYRYINFMSSGFPR--KLNRVEPLDALTWPLNLQKVF 393
0Y 432 LFKGARYY---VLAAGLOVEBPYPRLSD-WGIIPEEVSGLPPRDSIIFRDDRYYR 487
Db 394 LFKSGGYQWDELATFDS---SYKPIKGLFTGVNDSALMSNQDGRVYEFKCKYWR 450
0Y 488 LDOALQATTSGRNATELPMWGC 510
Db 451 LNQ-QLRVEKGYPRNISHNMHC 472

```

RESULT 2

NMatrix metalloproteinase 15 (EC 3.4.24.-) membrane type precursor - human
 A:Alternate names: membrane-type matrix metalloproteinase 2 (MT2MMP); MMP15
 C:Species: Homo sapiens (man)
 C:Date: 17-May-1996 #sequence
 C:Accession: I38029, G00041
 R:Will, H.; Hinzmann, B.
 Eur. J. Biochem. 231, 602-608, 1995
 A:Title: cDNA sequence and mRNA tissue distribution of a novel human matrix metalloproteinase
 A:Reference number: I38028, MUID:J95J77289, PMID:7649159
 A:Accession: I38029
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-669 <Mtl>
 A:Cross-references: UNIPROT:P5151, EMBL:Z48482, NID:G963055, PIDN:CAA88372.1, PID:G963055
 R:Seiki, M.
 submitted to GenBank, July 1996
 A:Reference number: H00041
 A:Accession: G00041
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 106-608, 'R', 610-669 <SRI>
 A:Cross-references: GB:D86331; NID:G1418214; PIDN:BAAL3071.1, PID:G1418215
 C:Genetics:
 A:Gene: GDB:MMP15; MT2-MMP
 A:Cross-references: GDB:642246
 C:Superfamily: Interstitial collagenase, hemopexin repeat homology; matrix metalloproteinase
 C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen
 F:1-41/Domain: signal sequence #status predicted <SIG>
 F:42-125/Domain: activation peptide #status predicted <ACT>
 F:79-304/Domain: matrix metalloproteinase homology <MMP>
 F:133-669/Product: matrix metalloproteinase 15 #status predicted <MAT>
 F:364-559/Domain: hemopexin repeat homology <PNX>
 F:664-664/Domain: transmembrane #status predicted <TRM>
 F:111-259, 263, 269/Binding site: zinc, catalytic (Cys, His, His, His, His, His) (inhibited) #status predicted
 F:150/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:259, 263, 269/Binding site: zinc, catalytic (His) (active) #status predicted
 F:260/Active site: Glu #status predicted

Query Match	18.8%	Score 534	DB 2	Length 669
Best Local Similarity	27.4%	Pred. No. 1.7e-26		
Matches 167	Conservative 64	Mismatches 102	Indels 172	Gaps 21
QY	9	LRLAQILLMGHLDAPAEERGOELRKEAEAFLEKGYGLNEQVKAPTSR-----PSDAI	63	
DB	29	LEFLLLVLTGCLGLGVA---AEDAENVAEHMLLTYGLTPQ--PSRIMSTKRSQIIASXL	83	
QY	64	RAQWWSQLPVSGVLDRAITLKQTRPRCGYTTDINSYAAMERISDLFAHRTIKMRKKRF	123	
DB	84	AEMQRRTYGLPVGVLDDEETKEMKPRRCGVPD-----QGVYK-----ANLRRRRKRY	132	
QY	124	AKQGNKMYKQHLSTYRLVNNPEHLRSQFAGPCAPSSCATSQRMWSSGRPQQAPELTSSG	183	
DB	133	ALTRGRMNNHLLFSTQNTYEKL-----	155	

```

Qy      184  PSKGTITMG-----AMFLMAQAQPMRTPLPR-----213
Db      156  -----GMTHSMEAVRAFRVWEQATPLFQEVPEYEDIRLRQKENDIVLPSAGFH 206
Qy      214  -----GEAFPDODERSLSRR--RGNLFLVYLAHEIGHTLG 247
Db      207  GDSPSPDGTGFLAHAYFPFGPLGGDTHFDADPEPTFSTDLHGNNLFLVAVHELGHYLG 266
Qy      248  LHSRPARPLMAYKKRLGRDAL-LSWDVLAVGSLYKPKLG-----GSVAVLQK 298
Db      267  LHSNSPNALIMPFYQKMDVNFKLPEDDLRGIQOLYGTGPGQPGQPTGPLTVTPRRRGR 326
Qy      299  LFTDEETWDSYSPQ-----GRRPQCGKYGCHSAPDALT 333
Db      327  F-----DHRPRPRQPRPPGCKRERPRKGRPVQRPQATRPRQYCGNIDCGDFTVAM 379
Qy      334  DRQOOLYIFKSGHEFEVADGNVSE-PRPLQERWVGLPRPNIAAAVSLNDGFFYFKGGR 392
Db      380  LR-GMFPFKGWMFRVHNRVLNDYPMPIGHFPRGLPGDI-SAAAYERQDGRFVFFKGDR 437
Qy      393  CWRFGPRKPVWGLRP-LGRAG-GLP-RHPRDALFPPLRLILFKGARYTVLAAAGLQVE 449
Db      438  YWLFREALEEGCYROPPLTSYGLGIPYDRIDALIMWELPGHTFFQEDRYKRMFNEETORG 497
Qy      450  FYPRSLDWMGGIPEEVSGALPRPDGS-IIFPRDRYWLRLDQAKTLTGSGRWATELPM 508
Db      498  FGYPFLISVMGIDIPASPKGAFLSNDAAVYTFYKOTKTKWKFDNEBLRMEPRGPKSLRDPM 557
Qy      509  GCM-HANGS 516
Db      558  GCGHVEBP 566

```

RESULT 3

matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - rat
N:Alternate names: membrane-type metalloproteinase
C:Species: Rattus norvegicus (Norway rat)
C:date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I84471; E16946
R:Okada, A.; Bellocq, J.P.; Rouyer, N.; Chénard, M.P.; Rio, M.C.; Chambon, P.; Basset, P.
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A:title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal ce
A:reference number: I38046; NCID:95224014; PMID:7708715
A:Accession: I84471
A:status: preliminary; translated from GB/EMBL/DBJ
A:molecule type: mRNA
A:Residues: 1-582 <RES>
A:cross-references: UNIPROT:Q10739; EMBL:X83537; NID:G805012; PIDN:CAA6521.1; PID:G8050
A:Accession: I61946
A:status: preliminary; translated from GB/EMBL/DBJ
A:molecule type: mRNA
A:Residues: 1-67, 'W', 69-254, 'A', 256-582 <RES>
A:cross-references: EMBL:X91785; NID:g1001926; PIDN:CAA62897.1; PID:g1001927
C:Genetics:
A:Gene: mt-mmp
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:1-23/Domain: signal sequence #status predicted <Sig>
F:24-97/Domain: activation peptide #status predicted <Pro>
F:61-284/Domain: matrix metalloproteinase homology <MMP>
F:313-508/Domain: hemopexin repeat homology <PN>
F:239, 243, 249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status }
F:239, 243, 249/Binding site: zinc, catalytic (His) (active) #status predicted
F:240/Active site: Glu #status predicted

Query Match	18.3%	Score 517.5	DB 2	Length 582
Best Local Similarity	29.5%	Pred. No. 2.5e-31		
Matches 152	Conservative 71	Mismatches 209	Indels 83	Gaps 20
QY	37	EAPLEKGY-----LNEQVPKAPSTPSPDRIAFQWWSQLPVSGVLDRLATLRQMTTRRC	91	
		:	::	

Db 36 EAMLOOYGYLPPGDLRTHTORSPOS--LSAIAIAIORYFYGLVGTAKSDTKAMKRRPRC 93
Qy 92 GVTDNNSYAAMERISDLFARHRTQMR---RKRFPAQGNKKYKQHLSTYLVNWPENHLRS 148
Db 94 GVPD-----KRGTEIKANVRKRYALIGLKKQNHETICIONY----- 131
Qy 149 RQFAPCAPSPSCGATSQR-----WSSGRP-----OPADPLTSGSPSSKCTTM- 192
Db 132 -----TPKVGSEYATFEAIRKAFRWBSATPLRFREVEYAYIRGHEKQADIMILFABG 184
Qy 193 ---GNAMPLMAOGAPMTPLPR---RGEAHFPODERWSLSRR--RGRNLFYVLAHEIGT 245
Db 165 FHGSDTPDPEGGLAAHAFPGPNIGGDTHFDSAEWTVQNDLNGNDIFLVAHVELGHA 244
Qy 246 LGLTSPAPRALMAPYKRLG-RDALLSWDDVLAVOSLYGKPLGGSVAQLPGKIFTPDR 304
Db 245 LGLHNSNDPSDIMAIFYQMDTENFVLPPDDRRGIGQLYSGSGS-----PTKMPQQR 298
Qy 305 TWDYSV-POGRBPETQGPYCHSPDALTVDROOQLYIFKSHFMFV-----AADGNVSEP 359
Db 299 TTSRPSVPDKPRNPFTYGPNI CDGNFDTVAMLR-GEWFYKERMFMVRNNQVMDG---YP 354
Qy 360 RPLQGRWGLPKNIEAAVSLNDGPFYFKGGRCMRFRPKFVWGLPOLCR--AGLPRH 417
Db 355 MEIQGFWRGLPASIN-TAYERKDGKRFVFKGDKHWVFDASLEPGYPKIKELGRGLPTD 413
Qy 418 P-DALFFPPLRLILFKGARYVVLARGLQYEPYPRSLQDMGIPPEVSGALPRPDS 476
Db 414 KIDALLFMWPNCKTYFFRANKIYFRNEEPRAYDSEYPKIKIWMGIPESPRSGFMSDEV 473
Qy 477 I-IFPRDDRYRLDQALQATTSGRWATELPMWGC 510
Db 474 FTYFYKGNKYWMFNNOCKLKEPVGYPKSRALRWMDGC 508
RESULT 4
138028
matrix metalloproteinase 14 (EC 3.4.24.-) membrane type precursor - human
N/Alternate names: matrix metalloproteinase MMP14; membrane type matrix metalloproteinase
C/Spectrum: Homo sapiens (man)
C/Date: 17-May-1996 #sequence revision 17-May-1996 #ext_change 09-Jul-2004
C/Accession: 138028; G02274; 138046; S78011; S45341; S71384
R/W11, H./Hinzmann, B.
Eur. J. Biochem. 231, 602-608, 1995
A/Title: cDNA sequence and mRNA tissue distribution of a novel human matrix metalloprote
A/Reference number: 138028; MUID:95377289; PMID:7649159
A/Accession: 138028
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-582 <WILL>
A/Cross-references: UNIPROT:P50281; EMBL:248481; NID:g963053; PID:CAA8372.1; PID:g9630
R/Luo, G.
Submitted to the EMBL Data Library, November 1995
A/Reference number: H00963
A/Accession: G02274
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-582 <LUO>
A/Cross-references: EMBL:U41078; NID:g1127836; PID:AAA83770.1; PID:g1127837
R/Okada, A./Bellio, J.P./Rouyer, N./Chenard, M.P./Rio, M.C./Chabon, P./Basseet, F
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A/Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal ce
A/Reference number: 138046; MUID:95324014; PMID:7708715
A/Accession: 138046
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-7,'S',9-582 <OKA>
A/Cross-references: EMBL:X83535; NID:g804993; PID:CAA5519.1; PID:g804994
R/Selki, M.
submitted to the EMBL Data Library, January 1994
A/Reference number: S78011
A/Accession: S78011
A/Molecule type: mRNA

A/Residues: 1-7,'S',9-337,'K',339-582 <SEI>
A/Cross-references: EMBL:D26512; NID:g793762; PID:BA05519.1; PID:g793763
R/Sato, H./Takino, T./Okada, Y./Cao, J./Shinagawa, A./Yamamoto, E./Selki, M.
Nature 370, 61-65, 1994
A/Title: A matrix metalloproteinase expressed on the surface of invasive tumour cells.
A/Reference number: S45341; MUID:94286011; PMID:8015608
A/Accession: S45341
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-7,'S',9-188,'R',190,'A',192-267,'K',269-272,'H',275,'P',277-285,'KQ',288,
R/Sato, H./Kinoshita, T./Takino, T./Nakayama, K./Selki, M.
FEBS Lett. 393, 101-104, 1996
A/Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP)
A/Reference number: S71384; MUID:96397540; PMID:8804434
A/Accession: S71384
A/Molecule type: protein
A/Residues: 112-116 <SAM>
C/Genetics:
A/Genes: GDB:MMP14; MT1-MMP
A/Cross-references: GDB:375731; OMIM:600754
A/Map position: 14q11-14q12
C/Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C/Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen
F/1-23/Domains: signal sequence #status predicted <SIG>
F/24-97/Domains: activation peptide #status predicted <PRO>
F/61-284/Domains: matrix metalloproteinase homology <MMP>
F/98-582/Product: matrix metalloproteinase 14 membrane type #status predicted <MAT>
F/285-311/Domains: hinge #status predicted <HNG>
F/314-508/Domains: hemopexin repeat homology <EPN>
F/539-562/Domains: transmembrane #status predicted <TM>
F/93,'239',243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F/130/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F/240/Active site: Glu #status predicted
F/319-508/Dissulfide bonds: #status predicted
Query Match 18.2%; Score 514.5; DB 2; Length 582;
Best Local Similarity 29.7%; Pred. No. 4,2e-31;
Matches 150; Conservative 69; Mismatches 223; Indels 63; Gaps 18;
Qy 37 EAPLEKRYG----LNEOVPAKPTSTRSDAIRAQMVSQLPVSGVLDAITRQNTPRC 91
Db 36 EAMLOOYGYLPPGDLRTHTORSPOS--LSAIAIAIORYFYGLVGTAKSDTKAMKRRPRC 93
Qy 92 GVTDNNSYAAMERISDLFARHRTQMRKRFPAQGNKKYKQHLSTYLVNWPENHLRSRQF 151
Db 94 GVPD-----KRGTEIKANVRKRYALIGLKKQNHETICIONYTPKY----- 135
Qy 152 GAPCAPSPSCGATSQRWSGRP-----OPADPLTSGSPSSKCTTM-----GNAMPLMA 200
Db 136 -GEVATVEALIRKAPRWBSATPLRFREVEYAYIRGHEKQADIMILFABGFGDSTPRFG 194
Qy 201 OGAPMTPLPR---RGEAHFPODERWSLSRR--RGRNLFYVLAHEIGTGLTSPAPR 255
Db 195 ECGFLAAHYFFPGPNIGGDTHFDSAEWTVQNDLNGNDIFLVAHVELGHALEHSSDPS 254
Qy 256 ALMAPYKRLG-RDALLSWDDVLAVOSLYGKPLGGSVAQLPGKIFTPDRTDYSV-POG 313
Db 255 ALMAPYQMDTENFVLPPDDRRGIGQLYSGSGS-----PTKMPQQRITTSRPSVDPK 308
Qy 314 RRPETQGPYCHSPDALTVDROOQLYIFKSHFMFV-----AADGNVSEPRLOERWGL 369
Db 309 PKNPFTYGPNI CDGNFDTVAMLR-GEWFYKERMFMVRNNQVMDG---YPMIQGFWRGL 364
Qy 370 PNIEAAVSLNDGPFYFKGGRCMRFRPKFVWGLPOLCR--AGLPRH-DAALFFPP 426
Db 365 PASIN-TAYERKDGKRFVFKGDKHWVFDASLEPGYPKIKELGRGLPTDIDALLFMWP 423
Qy 427 LARLLFKGARYVVLARGLQYEPYPRSLQDMGIPPEVSGALPRPDSI-IFPRDXY 485
Db 424 NGKTYFFRANKIYFRNEEPRAYDSEYPKIKIWMGIPESPRSGFMSDEVFTYFYKGNKY 483

Qy 486 WRUDAKLQATTSGRWATELPMWGC 510
Db 484 WKFNNOXKLVKPEGYPSALRDMWGC 508

RESULT 5

stromelysin 3 (EC 3.4.24.-) - mouse
C/Accession: A44399
C/Species: Mus musculus (house mouse)
C/Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 10-Jul-1998
C/Accession: A44399
R/RefSeq: O.; Wolf, C.; Linacher, J.M.; Hutin, P.; Wendling, C.; Lemer, M.; Basset, F.
A/Title: The breast cancer-associated stromelysin-3 gene is expressed during mouse mammary
A/Reference number: A44399; MUID:93054930; PMID:1429845
A/Accession: A44399
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-492 <RES>
A/Note: sequence extracted from NCBI backbone (NCBI:117216)
C/Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprotease
C/Keywords: hydrolase; metalloprotease; zinc; zymogen
F/1-262/Domain: matrix metalloprotease homology <MP>
F/292-484/Domain: hemopexin repeat homology <PRO>
F/84-219,223,229/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F/219,223,229/Binding site: zinc, catalytic (His) (active) #status predicted
F/220/Active site: Glu #status predicted

Query Match 16.5%; Score 466.5; DB 2; Length 492;
Best Local Similarity 28.7%; Pred. No. 1.5e-27;
Matches 152; Conservative 62; Mismatches 218; Indels 97; Gaps 22;

Qy 2 VARGLLRA-----LQLLMGHLDAQ-----PAERGGCELRKEAE 37
Db 1 MAAPACLRKISGCLLPRLPLLLPLLLPLPMLARAPRSHRHRYKRR----- 53
Qy 38 APLEKGYLNEQVPAKPTSTRFSDAIRAFQWSQLPVSGVDRAITLRQMTTP-RGCVTDT 96
Db 54 -----LHAAALPNTLT-----VPASHWPS-PAGS-----SRPLRCGVDP- 88
Qy 97 NSYAAAEIRISD-LFRRHRTKRRKKRPAQGNKWKYKQHLSTRLVNMPEHLRSRQFQAPC 155
Db 89 -----LPVNLARN-----RQKRFVLSGGRNEKTDITRIILRFWQLVREQVOTV 134
Qy 156 APPSSCGATSORMSGRPPQAPLITSGSSSKGTTTWG---AMPMAOGAPMTTPLP- 211
Db 135 A-----EALQWSEVTPLTFTVEHGRADIMIDPARWDSQDNLPPDGGIILAHGFFPK 188
Qy 212 --RGEAHPDDEKRWLSRRGRNLFVLAHEIGTTLGLTSPAPRALMAYRGLGRDA 269
Db 189 THREDDVHFDEYDETWTIGDNGTDLQVAHEFGHVLQHTTAAKALMSFFY-TPRYPL 247
Qy 270 LLSMDVLAVQSLYKPLIGGSVAVALPCKLFTDETWDYSYPOGRBPETGPKYCHSSFD 329
Db 248 SLSPDRRGITHLGRP---QMTPTSPAPLTSSQAGTIDWEIALLEPETP-PDVCERSFD 303
Qy 330 AITVDRQOOLYIFKGSHEWEVAADGNVSE--PRLOGRWGLCPNITAAVSLNDGDFY 387
Db 304 AVSTIR-GELEFFAGFVWRLRS-GRLOPGVPLALASHHOGLSPPDAAEADA-QCQIWF 360
Qy 388 PKGRGCRFRGPKPVWGLPOLCRAG--GLPRHPDALFPPLRLILFKGARYYVLARAG 445
Db 361 FQGAQVWVYGEKFLDPAFLSKLGLQSPVHA-ALWVGSEKNIYFFRGQGYWRHNPRT 419
Qy 446 LOVEPYPRSLQDWGGLPEEVSGLPRPDSIIFPRDRIWRLOAKLO 494
Db 420 QRVNPNVPRSTDMRGVSEIDAFQDAEGYAVFLGHLYMKDPVKVK 468

RESULT 6
148673
matrix metalloprotease (EC 3.4.24.-) membrane type precursor - mouse

C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
C/Accession: 148673
R/Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P.
A/Title: Membrane-type matrix metalloprotease (MT-MMP) gene is expressed in stromal ce
A/Reference number: 138046; MUID:95224014; PMID:7708715
A/Accession: 148673
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-582 <RES>

A/Cross-references: EMBL:X83336; NID:9804999; PIDN:CA58520.1; PID:9805000
C/Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprotease
C/Keywords: hydrolase; metalloprotease; zinc; zymogen
F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-97/Domain: activation peptide #status predicted <PRO>
F/61-284/Domain: matrix metalloprotease homology <MP>
F/313-508/Domain: hemopexin repeat homology <PRO>
F/93-239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F/239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F/240/Active site: Glu #status predicted

Query Match 16.4%; Score 463.5; DB 2; Length 582;
Best Local Similarity 27.7%; Pred. No. 3e-27;
Matches 144; Conservative 73; Mismatches 211; Indels 91; Gaps 21;

Qy 37 EAPLEKGYLNEQVPAKPTSTR-----FSDAIRAFQWSQLPVSGVDRAITLRQMTTP 89
Db 36 EAMQGFYLV-----PRDDLTHQGRSPQTLASVIMAIQKGYLYLVKAVSEMTKMRPP 91
Qy 90 RCGVTDNNSYAAAEIRISDLPARRHRTKRR--RKKRPAQGNKWKYKQHLSTRLVNMPEHL 146
Db 92 RCGVDP-----KFGTEIKAVNRKRYALQGLKQNHNEITFCQNV----- 131
Qy 147 RSRQFQAPCAPSPSCGATSOR-----WSSGR-----QPAPLITSGSSSKGTTTW- 192
Db 132 -----TPKGEVATPEAIKARVWESATPLRFREVPAYVIRGHEKQADWILFP 182
Qy 193 -----GMAPLMAOGAPMTTPLP--RGEAHPDDEKRWLSRR--RGNLFLVLAHEIG 243
Db 183 EGIHGSTPDDGCGFLAAHYFPGPNIGDTHFDSAEPTVQNEIDLNGMDILVAVHEIG 242
Qy 244 HTGLTHSPAPRALMAYRGLG-RDALSLMDVLAVQSLYKPLIGGSVAVALPCKLFTD 302
Db 243 HNLGHSNDPSDINSFQMDNTEFVLPDDRIGTQOLYSSKGS-----PTKMPQ 296
Qy 303 PFTWDSYS-POGRBPETGPKYCHSSFDATVDRQOOLYIFKGSHEWEV---AADGVNS 357
Db 297 PRTTSRPSVDPKQAPVAGPNICDGNFTVAMLR-GEFVFKERLWVRNNQVMDG--- 352
Qy 358 EPRPLQERWVGLPNIIEAAVSLNDGDFYFKGRCW---RFRGPKPVWGLPOLCRAG 413
Db 353 YMPITGQWRKGLPAIN-TAVERKDGTFVFFKGDGMWCVESASLEPYAHIKELVR--G 409
Qy 414 LPRHP-DALFPPLRLILFKGARYYVLARGGLQVEPYPRSLQDWGGLPEEVSGLALPR 472
Db 410 LPSDKIDTALFMPVPRKTYFRGNKTYFRNEEPAVDSVETPKNKKVWGLPESRSGFMG 469
Qy 473 PDGSI-IFPRDRIWRLOAKLOATTSGRWATELPMWGC 510
Db 470 SDEVFTFYKGNKWKFNNOXKLVKPEGYPSALRDMWGC 508

RESULT 7
JC6197
stromelysin 3 (EC 3.4.24.-) - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C/Accession: JC6197
R/Okada, A.; Saez, S.; Mitsui, Y.; Basset, P.
A/Title: Rat stromelysin 3: cDNA cloning from healing skin wound, activation by furin and
A/Reference number: JC6197; MUID:97208872; PMID:9055814

A/Content: Skin wounds
 A/Accession: JG6197
 A/Molecule type: mRNA
 A/Residues: 1-491 <OKA>
 A/Cross-references: UNIPROT:P97568; GB:U46034
 A/Comment: This protein is a member of the matrix metalloproteinase family.
 C/Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprote
 C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
 P/52-261/Domain: matrix metalloproteinase homology <MMP>
 P/291-483/Domain: hemopexin repeat homology <PXX>
 F/84-218, 222, 228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F/219, 222, 228/Binding site: zinc, catalytic (His) (active) #status predicted
 F/219/Active site: Glu #status predicted

Query Match 16.3%; Score 463; DB 2; Length 491;
 Best Local Similarity 29.2%; Pred. No. 2, 7e-27;
 Matches 153; Conservative 59; Mismatches 232; Indels 80; Gaps 22;

QY 2 VARVGLLRA-----LQLLMGH--DAQPERGGQELRKAFALEKGY 45
 DB 1 MARAACTLRRAISALLPLRLILLRLPPQLMADRRPENRRHPRVKVPQLP--AA 58
 QY 46 LNEQVFKAPTSTRFSDAIRAFQWVSQLPVSGVLDRAATLRQMTRP--RCGVTDITNSYAAWAE 104
 DB 59 LPMSLTSVPAS-----HIVPG-PASS-----SRPLRGVDPDPDV----- 92
 QY 105 RISDLFAHRTKMRKKRPAKQGNKYKQHLSTRLVNPENHLRSQGFACAPSSCGAT 164
 DB 93 -----LNAARN-----RQKRFVLSGGRWEKTDLTYYRIILFPWQLVREQVQTVA-----EA 137
 QY 165 SQWSSSGRPPQAPRLTSGSSSKGTTMGV---AMPMAQAGAPWRPFLE---RRGEAH 218
 DB 138 LRAWSEVTLPTFTVEHGRADIMIDFRVWNGDLPFDGEGILAAAFPKTHREGDVH 197
 QY 219 DQDERSLSRRRGNLFVLAHEIGTGLTHSPAPRALMAPYKRLGRDALISWDVLA 278
 DB 198 DYBETITIG-DKGTDLQVAHHEGHLGLOHTTAALMAISPFY-TRRYPLSLSPDDR 255
 QY 279 VQGLYKPKLQGSVAVALPGKLTDFETWDSYSPQGRRPETQGRKYCHSSFDALITVDROQ 338
 DB 256 IQLHYGRP---QLPTSPPTLTSSQAGTDITNELALQSEVP--PEVCESTSPDAVSTIR-GE 310
 QY 339 LITFKSGHFWGVADAGVSE--PRPLERVVGLPNTIEAANVSLNDQDFPFKGRGCMRF 366
 DB 311 LFFPKAGFVWRLLS-GQLQPCYPLASRHHQGLSPVDAAFEBA-QQIWFPGQAQVWY 368
 QY 397 RGRPRVWGLPOLCRAG--GLPRHPDALFPPLRLILFKGARYVVLARGLQVEPYPR 454
 DB 369 DGEKPVLPAPLSTLGIQGSVVAH-ALVWGEKKKIIFFRGQDVWRHPRTORVDNVP 427
 QY 455 SLQDMGIPREVSGALRPDGSIIFFRDRYWRLLDQAKLQATTS 498
 DB 428 RTTDMRGVPSBIDAFODAEGYAFVLRGHLWKFPDVKVLTES 471

RESULT 8
 813423
 stromelysin 3 (EC 3.4.24.-) precursor - human
 N/Alternate names: matrix metalloproteinase 11 (MMP11)
 C/Species: Homo sapiens (man)
 C/Date: 18-Feb-1994 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
 C/Accession: S13423; I38250; S58912
 R/Basset, P.; Bellocq, J.P.; Wolf, C.; Stoll, I.; Huttin, P.; Limacher, J.M.; Podhajcer,
 Nature 348, 699-704, 1990
 A/Title: A novel metalloproteinase gene specifically expressed in stromal cells of breast
 A/Reference number: S13423; MUID:91080920; PMID:1701851
 A/Accession: S13423
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-488 <BAS>
 A/Cross-references: UNIPROT:P24347; EMBL:X57766
 R/Argland, P.; Meiot, T.; Guerin, E.; Thomas, G.; Basset, P.
 J. Biol. Chem. 270, 20337-20344, 1995

A/Title: Structure and promoter characterization of the human stromelysin-3 gene.
 A/Reference number: I38250; MUID:95386471; PMID:7657606
 A/Accession: I38250
 A/Status: preliminary; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-36 <RS>
 A/Cross-references: EMBL:X84664; NID:g984746; PIDN:CA59150.1; PID:g987949
 R/Pei, D.; Weiss, S.J.
 Nature 375, 244-247, 1995
 A/Title: Furin-dependent intracellular activation of the human stromelysin-3 zymogen.
 A/Reference number: S58912; MUID:95265105; PMID:7746527
 A/Accession: S58912
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 81-101 <PEI>
 C/Genetics:
 A/Gene: GDB:MMP11; STWY3
 A/Cross-references: GDB:128630; OMIM:185261
 A/Map position: 22q11.2-22q11.2
 C/Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprote
 C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
 P/48-258/Domain: matrix metalloproteinase homology <MMP>
 F/488-480/Domain: hemopexin repeat homology <PXX>
 F/80, 215, 219, 225/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F/215, 219, 225/Binding site: zinc, catalytic (His) (active) #status predicted
 F/216/Active site: Glu #status predicted

Query Match 16.1%; Score 455.5; DB 2; Length 488;
 Best Local Similarity 30.0%; Pred. No. 9, 8e-27;
 Matches 136; Conservative 51; Mismatches 202; Indels 65; Gaps 17;

QY 68 WVSQLPVSGVLDRAAT-----LRQMTPRCGVTDITNSYAAWAEISDLFAHRTKMRKK 121
 DB 51 WHAALSSPARATQEARPPASLAPRPGVDPD-----DGLSARN-----RQK 96
 QY 122 RPAKQGNKYKQHLSTRLVNPENHLRSQGFACAPSSCGATSQWSSGRPPQAPLTS 181
 DB 97 RFLVSGGRWEKTDLTYYRIILFPWQLVREQVQTVA-----EALKWSDVTPLTFEVE 150
 QY 182 GSPSSKGTITMGV---AMPMAQAGAPWRPFLE---RRGEAHQDERWSLSRRGRNLF 235
 DB 151 GRADIMIDPARVWDGDLFPDGGEGILAAAFPKTHREGDVHIDYDWTGIDQGTDL 210
 QY 236 VVLAHEIGTGLTHSPAPRALMAPYKRLGRDALISWDVLAVALQSLYGRP----- 286
 DB 211 QVAHHEGHLGLOHTTAALMAISAFY-TRRYPLSLSPDCRGVQHLYGQRPWTVSRT 269
 QY 287 -LGSVAVALPGKLTDFETWDSYSPQGRRPETQGRKYCHSSFDALITVDROQIYIFKGS 345
 DB 270 ALGPQAGI-----DTNELAPLPDAP-PDACEASPDVASTIR-GEIIFPKAG 314
 QY 346 HFWGVADAGVSE--PRPLERVVGLPNTIEAANVSLNDQDFPFKGRGCMRFGRPVW 403
 DB 315 FVWRLLRG-GQLQPCYPLASRHHQGLSPVDAAFEBA-QQIWFPGQAQVWYDGEKPV 372
 QY 404 GLPOLCRAGGLPRHP-DAALFF--PPLRLILFKGARYVVLARGLQVEPYPSLQDMG 461
 DB 373 GPAPLTLL-GLVFPVVAALVWGEKKKIIFFRGQDVWRHPRTRVDSVPRRATW 431
 QY 462 IPREVSGALRPDGSIIFFRDRYWRLLDQAKLQ 495
 DB 432 VPSBIDAFOADQVAFVLRGRLYWKFPDVKVKA 465

RESULT 9
 KCMS51
 stromelysin 1 (EC 3.4.24.17) precursor - mouse
 N/Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); p
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Sep-1992 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
 C/Accession: J01476; S18867; B32963; S33139
 R/Hammani, K.; Henriet, P.; Beckhout, Y.
 Gene 120, 321-322, 1992

Db 309 -FKDHFMR-----KSURTEPEPEYLIISCFWPSLPSNMDAVEYTNEDTVEIFKGNQFMAL 363

Oy 397 RGRKRWGIGPOLCRAGLP---RHPDPAFFPPLRLRLIFKGRYYVLAAGGLOVEYYR 453

Db 364 RGHSEIADYPPKSIHTLGLPATVKKIDDAISNNEKRTTYFVEKKYRPFDEKKSMEGFP 423

Oy 454 RSL-ODMGCIPEEVSGLPRPDGSIIFPRDNRKRYMRDQAKLTATTSGRWATEL-----PVM 508

Db 424 RKIADFGVDSRVD-AVFEARGFLLYFSS-----GSSQLFEEDPPAKKVTHTLKSNSWF 475

Oy 509 GC 510

Db 476 NC 477

RESULT 10

KCRTH

stromelysin 1 (EC 3.4.24.17) precursor - rat

N/Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); P

C/Species: Rattus norvegicus (Norway rat)

C/Date: 13-Aug-1986 novecigus (Norway rat)

C/Accession: A00997; P0150; S2267

R/Matrisian, L.M.; Glaichenhaus, N.; Gesnel, M.C.; Breachnach, R.

EMBO J. 4, 1435-1440, 1985

A/Title: Epidermal growth factor and oncogenes induce transcription of the same cellula

A/Reference number: A00997, MUID:85284930, PMID:3875482

A/Accession: A00997

A/Molecule type: mRNA

A/Residues: 1-475 <MA1>

A/Cross-references: UNIPROT:P03957; GB:X02601; NID:957460; PTDN:CM26448.1; PID:G57461

R/Unenishi, F.; Yasumitsu, H.; Ashida, Y.; Yamauchi, J.; Umeda, M.; Miyazaki, K.

J. Biochem. 108, 537-543, 1990

A/Title: Purification and properties of extracellular matrix-degrading metallo-proteina

A/Reference number: P0150; MUID:91154156; PMID:1963430

A/Accession: P0150

A/Molecule type: protein

A/Residues: 19-20,'X',22-28,'110-112','X',114-115,'X',117,'X',119;309-325 <ME>

R/Breachnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.

Nucleic Acids Res. 15, 1139-1151, 1987

A/Title: Sequences coding for part of oncogene-induced transin are highly conserved in a

A/Reference number: A26403; MUID:87146421; PMID:3547333

A/Contents: annotation; introns

A/Note: Intron positions were determined by comparison of the previously reported cDNA s

J. Sanchez-Lopez, R.; Nicholson, R.; Gesnel, M.C.; Matrisian, L.M.; Breachnach, R.

J. Biol. Chem. 263, 11892-11899, 1988

A/Title: Structure-function relationships in the collagenase family member transin.

A/Reference number: S2267; MUID:88298869; PMID:2841336

A/Contents: annotation; active site; activation

A/Note: molecules with mutations in the autoinhibitory region showed a much increased te

R/Park, A.J.; Matrisian, L.M.; Kellis, A.F.; Pearson, R.; Yuan, Z.; Navre, M.

J. Biol. Chem. 266, 1584-1590, 1991

A/Title: Mutational analysis of the transin (rat stromelysin) autoinhibitor region demon

A/Reference number: A4028; MUID:91107652; PMID:1988438

A/Contents: annotation; autoinhibitory region

A/Note: Arg-89 and Cys-92 are essential for maintaining latency

C/Comment: This enzyme degrades various extracellular matrix proteins, including fibronect

C/Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment withcl

C/Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation

C/Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of whic

C/Genetics:

A/Introns: 33/3; 115/2; 165/1; 207/1; 262/1; 310/2; 355/1; 408/2; 443/1

C/Function:

A/Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl sit

C/Keywords: calcium; extracellular collagenase; hemopexin repeat homology; matrix metalloprotei

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-475/Product: prostromelysin #status predicted <SIG>

F:18-97/Domain: activation peptide #status predicted <PRO>

F:18-267/Domain: activation peptide #status predicted <ACT>

F:88-95/Region: autoinhibitory

F:88-95/Region: matrix metalloproteinase homology <MMP>

F:98-475/Product: stromelysin 1 #status predicted <MAT>

F:282-475/Domain: hemopexin repeat

F:90,216,220,226/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F:118/Binding site: carboxypeptidase (Asn) (covalent) #status predicted
 F:216,220,226/Binding site: zinc, catalytic (His) (active) #status predicted
 F:217/Active site: Glu #status experimental
 F:288-475/Diulfide bonds: #status predicted

Query Match 15.1%; Score 427; DB 1; Length 475;

Best Local Similarity 28.1%; Pred. No. 1,4e-24;
 Matches 142; Conservative 69; Mismatches 203; Indels 92; Gaps 20;

```

QY 9 LRLALQLLLM-----GHLDAPAEKGGDELKREAEAPLEKRYGYLNEQVPAKASTRFS 60
D 1 MKGLPVLMLCTAVCSSYPLHSGEEDAGMEVLRK-----YLENYGLKDVYQVFKKXSS 56
QY 61 DALRPFVWSQ---LPVSGVLDRAATLQMPRPFGVTDNTSYAAMARISDLFARHRTM 117
D 57 PVVKKIKQEMOKFLGLKMTGKLDSTMTBLMKPRGVPDVGSGTFP----- 101
QY 118 RRRKRFPAKQGNKMYKQHLSTYRLVNMPEHLRSRQFGAPCAPSSCGATSGR-----WSSGRP 173
D 102 -----PGSPKMKKMHISRIYVYTDL-----PRESVDSALERALKWMEVTP 144
QY 174 QPAPLITSGSPS---SKGTTTGWAMP-LMAQAPWRTFPLP---RGEAPFDODERWSLS 227
D 145 LTFERISGEADIMISPAVEEHGDFIPDGGVTLAAHAYAPGPGTNGDAHFDDEBWT-D 203
QY 228 RRRRRRNLPVLAHEIGTTLGITHSPAPRALMAPYTKR---LGRALLSKMDVLAVOSLYG 284
D 204 DVTGTNLFVLAHHLGSHLSLGFHSANAEALMYPYKSTDLAR-FHLSQDDVDIGISLYG 262
QY 285 KPLGGSVAVOLPGKLTDFETWDSYSPQGRRPETQPKYCHS--SFDAITVDROOQLYIF 342
D 263 PPTSSPDVTVPTK-----SNSLDPELT--PMCSALSFDVSTLRGEVLP-F 307
QY 343 KGSHEWEVAADGNVSEPRP---LQERWVGLPNIIEAAVSLNDGDFPFKGGCWRFPKRG 398
D 308 KDRFWMR---KSLRTPRPGFYLLSSFWPSLPNNMDAAYEVYTRNDYVILKGNQIMAIRG 363
QY 399 PKPFWGLPQLCRAGLP---RHPDALLFPPLRLILFKARYVYVLARGLQVPEYPRRS 455
D 364 HEELAGYPKSITHLGLPETYKIDALISLKDKQKTYFVEDKFWRFDEKSKMDPEPRK 423
QY 456 L-ODMGIPREVSGLPRPDGSIIF 480
D 424 IAEFPPIGTVD-AYFEAFGLYIF 448

```

RESULT 11

A53711
 collagenase 3 (EC 3.4.24.-) - human
 N/Alternate names: matrix metalloproteinase 13 (MMP13)
 C/Species: Homo sapiens (man)
 C/Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
 C/Accession: A53711
 R/Ref1fe, J.M.P.; Dier-Teza, I.; Balbin, M.; Sanchez, L.M.; Blasco, R.; Tollivia, J.; Lopez, J. Biol. Chem. 269, 16766-16773, 1994
 A/Title: Molecular cloning and expression of collagenase-3, a novel human matrix metalloproteinase
 A/Reference number: A53711; MUID:94266894; PMID:8207000
 A/Accession: A53711
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-471 <FRS>
 A/Cross-references: UNIPROT:P45452; GB:X75308; NID:9516385; PIDD:CA53056.1; PID:9516386
 C/Genetic8:
 A/Genes: GDB:MMP13; CLOC3
 A/Cross-references: GDB:373966; OMIM:600108
 A/Map position: 11q22.2-11q22.3
 C/Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprotease
 C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F:64-267/Domain: matrix metalloproteinase homology <MMP>
 F:276-471/Domain: hemopexin repeat homology <PXN>
 F:96,222,226,232/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F:222,226,232/Binding site: zinc, catalytic (His) (active) #status predicted

F:223/Active site: Glu #status predicted

Query Match 15.0%; Score 426.5; DB 2; Length 471;
 Best Local Similarity 30.0%; Pred. No. 1.5e-24;
 Matches 151; Conservative 55; Mismatches 204; Indels 93; Gaps 19;

```

QY 8 LRLALQLLLMGHLDAPAEKGGDE--LRKEAEAPLEKRYGYLNEQVPAK 54
D 5 VLAAPFLPSWTHCRALPLPSGDEDDLSIEDLQFAEYRLSYHPTNLAILKENAASM 64
QY 55 TSTRFSALTAFAQWQGLPVSGLDRAATLQMPRPFGVTDNTSYAAMARISDLFARH 114
D 65 T-----ERLEKQSPFGLVETGKLDVTLDMKKPRGVPDVGEBVFPRTL----- 111
QY 115 TKRRKKRPAKQGNKMYKQHLSTYRLVNMPEHLRSRQFGAPCAPSSCGATSGRWSGR 173
D 112 -----KSKNKLTYRIYVYTDTHSE-----VEKAFKAAPKWSDVTP 150
QY 174 QPAPLITSGSPS---SKGTTTGWAMP-----LMAQAPWRTFPLPRGEAPFDODERW 224
D 151 INFTRLHDGIADIMISFGIKRHGDFYPDGPGLAHAFP---FGPNYGGDAHFDDEBWT 207
QY 225 SLRRRRRNLPVLAHEIGTTLGITHSPAPRALMAPYTKRGLRD-ALLSMDVLAVOSLY 283
D 208 T-SSSKGYNLFVLAHHEFGSHSLGDSKDKALMFPITYTYSKSHFWLPDDVQIGISLY 266
QY 284 GKPLGGSVAVOLPGKLTDFETWDSYSPQGRRPETQPKYCHS--SFDAITVDROOQLYI 341
D 267 G-----PG-----DEPNRKHPT--PDGCDPSLSDAITSRLGERM-I 302
QY 342 KGSHEWEVAADGNVSEPRP-LQERWVGLPNIIEAAVSLNDGDFPFKGGCWRFPKRP 401
D 303 FKORFFRLHPHQVDALFLTKSPWPLPRIDAAVSHPSHDLIFIRGKRFLALNGDI 362
QY 402 VMGLPQLCRAGLPFRH---DAALFPPLRLILFKARYVYVLARGLQVPEYPRSL-Q 457
D 363 LEQYPKKISEGLSEKVEKYSAAVHFEDTGKTLFSGNQVWRVDDTNHMDKDPRLIE 422
QY 458 DMGIPREVSGLPRPDGSIIF 480
D 423 DFEIGDKVD-AYEKKGYIIF 444

```

RESULT 12

KCRS2
 etromelysin 2 (EC 3.4.24.22) precursor - rat
 N/Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C/Accession: B26403; A41775; S26498
 R/Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.
 Nucleic Acids Res. 15, 1139-1151, 1987
 A/Title: Sequences coding for part of oncogene-induced transin are highly conserved in
 A/Reference number: B26403; MUID:87146421; PMID:3547333
 A/Accession: B26403
 A/Molecule type: mRNA
 A/Residues: 1-476 <BBE>
 A/Cross-references: UNIPROT:P07152; EMBL:X05083; NID:957388; PIDD:CAA28739.1; PID:95738
 A/Note: Intron positions were determined by comparison of the cDNA sequence to genomic
 A/Note: mRNA for this protein was expressed in several transformed rat embryo fibroblasts
 R/Chan, J.C.; Scanlon, M.; Zhang, H.Z.; Jia, L.B.; Yu, D.H.; Hung, M.C.; French, M.; Bai
 J. Biol. Chem. 267, 1099-1103, 1992
 A/Title: Molecular cloning and characterization of V-mos-activated transformation-ssboc
 A/Reference number: A41775; MUID:92112740; PMID:1370458
 A/Accession: A41775
 A/Molecule type: mRNA
 A/Residues: 1-476 <CHA>
 A/Cross-references: GB:M65253; NID:9207150; PIDD:AAA42202.1; PID:9207151
 A/Note: sequence extracted from NCBI backbone (NCBI:P:76184)
 R/De Young, M.W.; Mukherjee, B.B.
 Oncogene 7, 109-119, 1992
 A/Title: Transformation of normal rat kidney cells by v-K-ras enhances expression of tr
 A/Reference number: B26496; MUID:92156347; PMID:1741158

A:Accession: S26498
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 31-103, 'L', 241-242, 'TOMEKPR', 251, 'L', 253-254, 'GE', 293-294, 'L', 296 <DEV>
A:Cross-references: EMBL:X64020
C:Genetics:
A:Intons: 35/3; 117/2; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1
C:Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-476/Domain: propeptide sequence #status predicted <PRO>
F:18-99/Domain: propeptide sequence #status predicted <ACT>
F:60-264/Domain: activation peptide #status predicted <ACT>
F:90-97/Region: autocatalytic domain #status predicted <AMP>
F:100-476/Region: autocatalytic domain #status predicted <AMP>
F:1283-476/Domain: hemopexin repeat homology <MAT>
F:202, 218, 222, 228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:120/Binding site: carbonyl site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:218, 222, 228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:289-476/Disulfide bonds: #status predicted

Query Match 15.0%; Score 425.5; DB 1; Length 476;
Best Local Similarity 28.8%; Pred. No. 1.8e-24;
Matches 152; Conservative 59; Mismatches 237; Indels 79; Gaps 19;

QY 9 LRAIQLLMGLDQNP---AERGQELKEAEALFLEYGYL---NEQVPAKPTSTRPSDA 62
DB 4 LAIVLVCFLPCISVPLHGAVRDHSHTDLAQVLEKYNFRKNEKQFFPKKSSPVYKK 63
QY 63 IRAFQWVSQPLVSGVLDRLATLQMTPRCGVTDNSYAAMERISDLFAHRTMKRRKR 122
DB 64 IEMQKFLGLEMTGKLDNSNTVMHMKRCVDPVGGSTP----- 103
QY 123 FAKGKNWYKOHLSYLVNMPENHRSKRFQAPACPPSSCGATSOR---WSSGRPOQAP 178
DB 104 --PGSPKRNKHISYRIVNTYLDL-----PRESVDAIERLAKWEETPLTPSK 151
QY 179 LITGSPBS---SKGTTTGMAMPPLMAOGAPWRTPLR---RGAHFDODERMSLSRRGR 232
DB 152 ISEGDADIMISFAVGEHGDYFPDVGQSLAHAYPPGPGYGAHFDDEKSLIG-PSGT 210
QY 233 NLFLVLAHEIGTLGLTHSPAPRALMAPYKRLGRDA--LISWDVLAQSLYLG-KPLCG 289
DB 211 NLFVLAHEIGTLGLTHSPAPRALMAPYKRLGRDA--LISWDVLAQSLYLG-KPLCG 289
QY 290 SVAVOLPGKLTDFEWDYSYSPQGRPEYQGRYCHS--SPDAITVDROOQLYFKGSHF 347
DB 271 AIVVVP-----SVSP---KPEP---PVKCDPALSFDAVTMLGEPFLF-PKDNH 313
QY 348 WEVAADGNVSEPRPQERWGLPNNIEAASVSLNGDFFPYGSGCMFRFGKPYWGLPQ 407
DB 314 WRTQWNPBEPFHLISAFWPSLPSGLDAAYEANNKORVILFKGSGFMAVRGNEVQAGYPK 373
QY 408 LCRAGLP---RHPDALFPPPLRLILFKGARYVLAAGLOVEPYPRSL-ODMGIR 463
DB 374 RIHTLGFPPTVYKIDDAVFEKEKKKTYFFVGDKWRPDEFTRQMDKGFRLITDPGPIE 433
QY 464 BEVSGALPRPDGSIIFPRDRLDQAKLQATTSGRWATELPMWGC 510
DB 434 PQVDAVL-HAFGFYFPGSSQGFPPD---NARTVHTLXNSWILLC 476

RESULT 13

JC5743
matrix metalloproteinase (EC 3.4.24.-) precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 09-Dec-1997 #sequence_revision 23-Jan-1998 #text_change 09-Jul-2004
C:Accession: JC5743
R:Barlet, J.D.; Simmer, J.P.; Xue, J.; Margolis, H.C.; Moreno, E.C.
Gene 183, 123-128, 1996
A:Title: Molecular cloning and mRNA tissue distribution of a novel matrix metalloprotein
A:Reference number: JC5743, MUID:97149288; PMID:8996096

A:Accession: JC5743
A:Molecule type: mRNA
A:Residues: 1-483 <BAR>
A:Cross-references: UNIPROT:P79287; GB:U54825; NID:91800212; PID:AB41396.1; PID:91800
A:Experimental source: enamel organ
C:Comment: This enzyme plays a role in enamel biomineralization and development.
C:Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: hydrolase; metalloproteinase; zinc
F:1-23/Domain: signal sequence #status predicted <SIG>
F:23-483/Domain: matrix metalloproteinase #status predicted <MAT>
F:1283-476/Domain: hemopexin repeat homology <MAT>
F:290-483/Domain: matrix metalloproteinase homology <AMP>
F:100-483/Domain: hemopexin repeat homology <AMP>
F:226, 230, 236/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:227/Active site: Glu #status predicted

Query Match 14.5%; Score 410; DB 2; Length 483;
Best Local Similarity 28.5%; Pred. No. 2.7e-23;
Matches 143; Conservative 64; Mismatches 209; Indels 86; Gaps 21;

QY 36 AEAFLEKY-----GY-LNEQVPAKPTSTRPSDAIRAFQWVSQPLVSGVLDRLATLQMTTP 89
DB 41 AQAYLDKTYTKKGSHQVGEVNAKGS--MVKKIKELQAFGLRVTGKLDRTMDVYKRP 98
QY 90 RCGVTDNSYAAMERISDLFAHRTMKRRKRFAKQKNWYKOHLSYLVNMPENHRSR 149
DB 99 RCGVDPVANY-----RLPFGKMKKNITLYISKYTSM--- 133
QY 150 QFCAPCAPSSCGATSORWSSGRPOQAPLITGSPS---SKGTTTGMAMPPLMAOGAPWR 206
DB 134 ---TAEVDKAMEMALQAWSSAVPLSFVRVNAGEADIMISFETGHDGSPYDPGRGTLA 190
QY 207 TFFLPRR---GEAHPDODERMSLSRRGRNLFVLAHEIGTLGLTHSPAPRALMAPYK 263
DB 191 NAFAPGEGIGDTHFDNAEKMTWG--MGPNLFTVAHHEFGALGASHTDPSALMAYPYK 249
QY 264 RLGRDAL-LSMDVLAVALSYLGKPLGSGVAVALPGKLTDFEWDYSYSPQGRPEYQGR 322
DB 250 YQNPYGFHLPRDVKVGLQALYV-----PRKFTGKPT---VPHRPNNPSLPD 294
QY 323 YC--HSSPDAITVNRQOQLYFKGSHF--EVAADGNVSEPRPQERWGLPNNIEAASV 378
DB 295 ICSSSSGSDANTM-LGKELFFRDRITWRQVHLMSCI-PPSTTSSFPQLMSVDAAYE 352
QY 379 SLNDGDFYFFKGGCMFRFGKPYWGLPOLCRAGGLPRHP--DAALFPPPLRLILFKG 435
DB 353 VADRGMAYFFKGPYHWTTRGQ--MGSPRTIYDGFPRYQRIIDAAVHLKDTQKTLFVG 411
QY 436 ARYVLAAGLOVEPYPRSL-ODMGIRPESVSGALPRPDGSIIFPRDRLDQAK-- 492
DB 412 DEITYSDERKRNKDKYPKNTEEFSGVNGQIDAAV-ELNGYIYFSGPRAKYTDEKED 470
QY 493 ----LQATTSGRWATELPMWGC 510
DB 471 VVSLKNS-----WIGC 483

RESULT 14

A23685
interstitial collagenase (EC 3.4.24.7) precursor - rat (fragment)
N:Alternate names: matrix metalloproteinase 1 (MMP1); vertebrate collagenase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
R:Quinn, C.O.; Scott, D.K.; Brinckerhoff, C.E.; Mattiastian, L.M.; Jeffrey, J.J.; Partridge
U. Biol. Chem. 265, 22342-22347, 1990
A:Title: Rat collagenase. Cloning, amino acid sequence comparison, and parathyroid hormo
A:Reference number: A23685, MUID:91093077; PMID:2176215
A:Accession: A23685
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-466 <QUT>
A:Cross-references: UNIPROT:P23097; GB:M60616; GB:M36452; NID:9203498; PID:AA72124.1; I

C:Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprotease
 C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F:159-262/Domain: matrix metalloproteinase homology <MMP>
 F:123-466/Domain: hemopexin repeat homology <PXN>
 F:91,217,221,222/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F:217,221,222/Binding site: zinc, catalytic (His) (active) #status predicted
 F:218/Active site: Glu #status predicted

Query Match 14.4%; Score 407.5; DB 2; Length 466;
 Best Local Similarity 28.1%; Pred. No. 3,9e-23;
 Matches 147; Conservative 65; Mismatches 214; Indels 97; Gaps 20;

```

14 LLLMGLDADQAPERG---GQELRKE---AEAFLEKY-----GYLNEQVPKAPSTSRF 59
5 LLSWTHCWSLPLPYGDDDDDLSEEDLEFAEHYKSYHVPVTLAAIL-----KKSIVTST 59
60 SDAIRAFQVNSQLPVSGVLDRLATLRQMTPRCGVNTTNSYAAAEKISDLFAHRTRKMR 119
60 VRLRKMOSFFGIDVYTKLDDPTLDIRKPRCGVPVGVYVFPRTL----- 106
120 KRRFAKQGNKMYKQHLSTRLVNWPEHLSRQFGAPCAPSSCGATSGRMSGRPQAPL 179
107 -----KMSQTNLITVIVNTPTDISHSEV-----EKAPKAKKWSDVTPPLNFTRI 151
180 TSGSPS---SKGTTTGMAMP-----LMAQAPWETPPLPRRGAHPQDERWSLSRRR 230
152 HDGTADIMISFGTKEHGDFFPDGSGLLAHAPF---PGPNLGGADHPDDEFTWT-SSSK 207
231 GNNLPLVLAHEIGTHTGLTHSPAPRALMAYTKLRD-ALLSMQVYLAQSLYKPLGG 289
208 GNNLPLVLAHEIGHSIGLHSHKDPGALMPEPIYTTKSHFMLPDDVQGISLYG----- 262
290 SVAVALPGKLTDFETWDSYPSQGRREPQGRKCHS--SPDITVDRQOQLYIFKGSHP 347
263 -----PG-----DEDPNPKPKPT--PEKCDPALSLDAITLSRGETM-IFKDRFP 303
348 MEVAADGNVSEPRPLGERWVGLPNNIEAAVSLNDGDFYFKGRCWFRGPRPVNLQ 407
304 MRLHPQOVPELPLTGSFWPELPHNVDAAYEHPSRLMFLFRGRKFMALNGVDIMGYRR 363
408 LCRAGGLPRHP--DAALFPPLRLILKGAHYTLANGGLQVEYYRSL-QDWGGLP 463
364 KISDLFPKPVKRLSAVAHFEDTGKTLFPSSGNHWSYDADNQMDDYDRLIEEPPGIG 423
464 EEVSGALPRDGSIIIFPR-----DRIYRMLDQAKLQATTSGRW 501
424 DKVD-AVYERKGIYTFNCPIDPFISIMSNRIYVWPTNSLW 465

```

RESULT 15

JC6505
 etromelysin 2 (EC 3.4.24.22) precursor - mouse
 M:Alternate names: matrix metalloproteinase 10
 C:Species: Mus musculus (house mouse)
 C>Date: 16-Oct-1998 #sequence_rev15ion 16-Oct-1998 #text_change 09-Jul-2004
 C:Accession: J06505
 R:Madlener, M.; Werner, S.
 Gene 202, 75-81, 1997.
 A>Title: cDNA cloning and expression of the gene encoding murine etromelysin-2 (MMP-10).
 A:Reference number: J06505; M0ID:98087420; PMID:9427548
 A:Accession: J06505
 A:Molecule type: mRNA
 A:Residues: 1-476 <MAD>
 C:Cross-references: UNIPROT:O55133; GB:Y13185; NID:q2793311; PIDN:CAAT3641.1; PID:q27913
 C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin.

A:Gene: MMP-10

C:Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprotease
 C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-476/Product: proetromelysin 2 #status predicted <PRO>
 F:18-99/Domain: activation peptide #status predicted <ACT>
 F:60-264/Domain: matrix metalloproteinase homology <MMP>

F:90-97/Region: autoinhibitory
 F:100-476/Product: etromelysin 2 #status predicted <MAT>
 F:283-476/Domain: hemopexin repeat homology <PXN>
 F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F:120/Binding site: carbonyl (Asn) (covalent) #status predicted
 F:18,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
 F:219/Active site: Glu #status predicted
 F:289-476/Dileptide bonds: #status predicted

Query Match 14.3%; Score 406; DB 1; Length 476;
 Best Local Similarity 27.5%; Pred. No. 5.3e-23;
 Matches 138; Conservative 68; Mismatches 211; Indels 84; Gaps 19;

```

36 AEAFLEKYGL---NEQVPKAPSTSRFSDAIRAFQVNSQLPVSGVLDRLATLRQMTPRCG 92
34 AQQVLEKYVNFKNKQKIFKRKSSPVYKKIDEMQKFLGLMNTGKLDSTNLMELMKPRCG 93
93 VPTNLSYAAAEKISDLFAHRTRKMRKKRFAKQGNKMYKQHLSTRLVNWPEHLSRQFG 152
94 VPDVCGFSTF-----PGSPKMKKSHITVIVVY----- 121
153 APCAPSSCGATSQR---WSSGRPQAPLITSGSPS---SKGTTTGMAMPMLAQAPW 205
122 TPDLPRQVDSALRKALKEBEVTPLTSTRISGEADIMISPAVGEHGFYFDGFGSL 181
206 RTPLPR---RGAHPQDERWSLSRRRGNLFFVLAHEIGTHTGLTHSPAPRALMAYPY 262
182 AAAYPRGPFYGDVHFDDKKTLLA-PSGTNLFVLAHEIGHSIGLFIHSDKESLMTYRY 240
263 KRLGRDA--LISWDVLAQSLYK-PLGGSVAVALPCKLFTDFETWDSYSPQGRPEPQ 319
241 RSTSPANFHLQDDIEGIGSLYAGPSSDAIVVPL-----SVSP---RPEP- 285
320 GPKYCHS--SPDITVDRQOQLYIFKGSHPMEVAADGNVSEPRPLQERWVGLPNNIEAA 377
286 -PDKCDPALSFDSVSTLKEVLP-FKDRYFMRKSHMNEPETHLSAFNPTLPSDDAAY 343
378 VSLNDGDFYFKGRCWFRGPRPVNGLPOLCRAGGLP---NHPDPALEFPPLRLILPK 434
344 EAHNTDSVLIFFKGSQFMVNRGNEVQAGYKGIHTLGFPTVKIDAAYEKKKTYFFV 403
435 GARYVLAAGLQVEPYRSL-QDWGIIPEVSGALPRDGSIIFFPRDRYRLDQAKL 493
404 GDKYRFBETRYVMKGFPRQITDDPGIEPVDAVL-HEGFYFFFRGSSQFEFD----- 458
494 QATTSGRNATEL-----PMWGC 510
459 ---PNARTVTHILKSNWLLC 476

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Search completed: June 13, 2005, 18:02:32
 Job time : 43 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 13, 2005, 17:14:56 ; Search time 163 Seconds
(without alignments)
1233.637 Million cell updates/sec

Title: US-10-791-980-6

Perfect score: 2834
Sequence: 1 MVARVGLLRALQLLWGL.....WATLEPMWGCHWANGSALF 520

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1Dec04:*

1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2834	100.0	520	5 AAE14394	AAE14394 Human mat
2	2472	87.2	520	4 AAB74690	AAB74690 Human pro
3	2472	87.2	520	4 AAB85427	AAB85427 Human MPR
4	2472	87.2	520	4 AAU12243	AAU12243 Human PRO
5	2472	87.2	520	5 AAU79810	AAU79810 Novel mat
6	2472	87.2	520	5 ABG31460	ABG31460 Human mat
7	2472	87.2	520	6 AB017687	AB017687 Novel hum
8	2472	87.2	520	6 AB080941	AB080941 Human PRO
9	2472	87.2	520	6 AB066641	AB066641 Human PRO
10	2472	87.2	520	6 ABUS9722	ABUS9722 Novel sec
11	2472	87.2	520	6 AB024912	AB024912 Human sec
12	2472	87.2	520	6 AB066917	AB066917 Human sec
13	2472	87.2	520	6 ADA45663	ADA45663 Novel hum
14	2472	87.2	520	6 ADA76094	ADA76094 Human PRO
15	2472	87.2	520	6 ADA18744	ADA18744 Human PRO
16	2472	87.2	520	6 ADA61367	ADA61367 Homo sapi
17	2472	87.2	520	6 ADB19152	ADB19152 Novel hum
18	2472	87.2	520	6 ADB27653	ADB27653 Human PRO
19	2472	87.2	520	6 ADA86172	ADA86172 Novel hum
20	2472	87.2	520	6 ADB15736	ADB15736 Human PRO
21	2472	87.2	520	6 ADA47522	ADA47522 Human PRO
22	2472	87.2	520	6 ADA67317	ADA67317 Human PRO
23	2472	87.2	520	6 ADB30324	ADB30324 Human PRO
24	2472	87.2	520	6 ADA85620	ADA85620 Novel hum
25	2472	87.2	520	6 ADA96832	ADA96832 Human PRO

26	2472	87.2	520	6 ADA79136	ADA79136 Human PRO
27	2472	87.2	520	6 ADA87275	ADA87275 Novel hum
28	2472	87.2	520	6 ADB16477	ADB16477 Human PRO
29	2472	87.2	520	6 ADA91569	ADA91569 Novel hum
30	2472	87.2	520	6 ADB14632	ADB14632 Human PRO
31	2472	87.2	520	6 ADB18593	ADB18593 Novel hum
32	2472	87.2	520	6 ADB93808	ADB93808 Human PRO
33	2472	87.2	520	6 ADB19704	ADB19704 Novel hum
34	2472	87.2	520	6 ADB13016	ADB13016 Human PRO
35	2472	87.2	520	6 ABO43220	ABO43220 Novel hum
36	2472	87.2	520	6 ADA74270	ADA74270 Human PRO
37	2472	87.2	520	6 ADB24503	ADB24503 Human PRO
38	2472	87.2	520	6 ADA82027	ADA82027 Human PRO
39	2472	87.2	520	6 ADA74950	ADA74950 Human PRO
40	2472	87.2	520	6 ADA85068	ADA85068 Novel hum
41	2472	87.2	520	6 ADA84516	ADA84516 Novel hum
42	2472	87.2	520	6 ADB29772	ADB29772 Human PRO
43	2472	87.2	520	6 ADA80300	ADA80300 Human PRO
44	2472	87.2	520	6 ADA75542	ADA75542 Human PRO
45	2472	87.2	520	6 ADA46767	ADA46767 Human PRO

ALIGNMENTS

RESULT 1	AAE14394	standard; protein; 520 AA.
ID	AAE14394	
XX	AAE14394;	
AC	AAE14394;	
XX	AAE14394;	
DT	16-OCT-2002 (first entry)	
XX	16-OCT-2002 (first entry)	
DE	Human matrix metalloproteinase MMP10.	
XX	Human matrix metalloproteinase MMP10.	
XX	Matrix metalloproteinase; MMP; extracellular matrix; ECM;	
XX	embryonic development; morphogenesis; reproduction; tissue repair;	
KW	mental disorder; Alzheimer's disease; multiple sclerosis; obesity;	
KW	Parkinson's disease; motor neuron disease; metabolic disease; retinopathy;	
KW	type 2 diabetes; cardiovascular; dyslipidaemia; adipsogenesis; neuropathy;	
KW	neuropathy; proliferative disease; cancer; psoriasis;	
KW	prostate hyperplasia; hormonal disorder; alopecia; Crohn's disease;	
KW	central nervous system disorder; CNS; inflammatory condition; arthritis;	
KW	periodontal disease; wound healing; human; MMP10.	
XX		
OS	Homo sapiens.	
XX	Homo sapiens.	
XX	WO200190326-A2.	
XX	29-NOV-2001.	
XX	29-NOV-2001.	
XX	22-MAY-2001; 2001WO-US016563.	
XX	22-MAY-2001; 2001WO-US016563.	
XX	22-MAY-2000; 2000US-0206119P.	
XX	22-MAY-2000; 2000US-0206119P.	
XX	(PHAA) PHARMACIA & UPJOHN CO.	
XX	(PHAA) PHARMACIA & UPJOHN CO.	
XX	Holmgren E, Kihlen M, Wood T, Ekblom J;	
XX	Holmgren E, Kihlen M, Wood T, Ekblom J;	
XX	WPI; 2002-083105/11.	
XX	WPI; 2002-083105/11.	
XX	N-PSDB; AAD23965.	
XX	N-PSDB; AAD23965.	
XX	New matrix metalloproteinases (MMP) genes and polypeptides, useful for	
XX	treating diseases or for screening modulators of MMP to treat such	
XX	diseases, e.g. mental disorders, Parkinson's disease, cancers or	
XX	inflammatory conditions.	
XX	Claim 31; Page 60; 94pp; English.	
XX	Claim 31; Page 60; 94pp; English.	
XX	The invention relates to genes encoding matrix metalloproteinases (MMP).	
XX	The MMP genes are useful for producing MMP polypeptides and for screening	
XX	modulators of MMP. The MMPs are useful for breaking down extracellular	
XX	matrix (ECM), which is essential for processes including embryonic	

CC development, morphogenesis, reproduction, or tissue repair and
 CC remodeling. The MMPs are particularly useful for identifying compounds
 CC that modulate the activity of genes to treat pathologies, e.g. mental
 CC disorders, Alzheimer's disease, multiple sclerosis, Parkinson's disease
 CC or motor neuron disease. The MMP polypeptides and genes, as well as their
 CC modulators, are useful for treating metabolic diseases and disorders
 CC (e.g. type 2 diabetes, obesity, cardiovascular, dyslipidaemia,
 CC atherosclerosis, retinopathies, neuropathies or nephropathies),
 CC proliferative diseases and cancers (e.g. breast, colon or lung cancer,
 CC tumour growth, tumour invasion, psoriasis or prostate hyperplasia),
 CC hormonal disorders (e.g. male/female hormonal replacement, polycystic
 CC ovarian syndrome or alopecia), central nervous system (CNS) disorders,
 CC inflammatory conditions (e.g. Crohn's disease or arthritis), periodontal
 CC diseases or wound healing. The present sequence is human matrix
 CC metalloproteinase MMP10

XX
 SQ Sequence 520 AA;

Query Match 100.0%; Score 2034; DB 5; Length 520;
 Best Local Similarity 100.0%; Pred. No. 26-251;
 Matches 520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVARVGLLRALQLLMGHLDAQPAERGGOELRKEAEAFLEKYGYNLEQVPAPPTSTRS 60
 DB 1 MVARVGLLRALQLLMGHLDAQPAERGGOELRKEAEAFLEKYGYNLEQVPAPPTSTRS 60
 QY 61 DAIRAFQWYSQLPVSGVLDRAITRQMTPRCGVTDNTSYAAMERISDLFAHRRTKMRK 120
 DB 61 DAIRAFQWYSQLPVSGVLDRAITRQMTPRCGVTDNTSYAAMERISDLFAHRRTKMRK 120
 QY 121 KEPAQGNKWKYKQHLSTYLVNMPENHSRQFAPCAPPSSCGATSGRPSGRPOAPLIT 180
 DB 121 KEPAQGNKWKYKQHLSTYLVNMPENHSRQFAPCAPPSSCGATSGRPSGRPOAPLIT 180
 QY 121 KEPAQGNKWKYKQHLSTYLVNMPENHSRQFAPCAPPSSCGATSGRPSGRPOAPLIT 180
 DB 121 KEPAQGNKWKYKQHLSTYLVNMPENHSRQFAPCAPPSSCGATSGRPSGRPOAPLIT 180
 QY 181 SCSPSSKGTITGMAFPLMAQAPWRTPLPRGGEAFPODERMSLSRRRGNTLFFVLAH 240
 DB 181 SCSPSSKGTITGMAFPLMAQAPWRTPLPRGGEAFPODERMSLSRRRGNTLFFVLAH 240
 QY 241 EIGHTLGLTHSPAPALMAFYKRLGRNALMSWDVLAVALSYKPLGSAVAVOLPGKLF 300
 DB 241 EIGHTLGLTHSPAPALMAFYKRLGRNALMSWDVLAVALSYKPLGSAVAVOLPGKLF 300
 QY 301 TDFETWDSYSPQGRREPTEQPKYCHSSFDATVDRQOQLYTFKSHFEVNAADGVSEPR 360
 DB 301 TDFETWDSYSPQGRREPTEQPKYCHSSFDATVDRQOQLYTFKSHFEVNAADGVSEPR 360
 QY 301 TDFETWDSYSPQGRREPTEQPKYCHSSFDATVDRQOQLYTFKSHFEVNAADGVSEPR 360
 DB 301 TDFETWDSYSPQGRREPTEQPKYCHSSFDATVDRQOQLYTFKSHFEVNAADGVSEPR 360
 QY 361 PLOERWVGLPNTIEAAVSLNDGDFYFFKGGRCWFRGPKVWGLPQLCRAGGLPRHPDA 420
 DB 361 PLOERWVGLPNTIEAAVSLNDGDFYFFKGGRCWFRGPKVWGLPQLCRAGGLPRHPDA 420
 QY 421 ALFFPPLRLILFKGARVYVLARGLQVEPYPPSLQWGGIPREVS GALPRPGSIITFP 480
 DB 421 ALFFPPLRLILFKGARVYVLARGLQVEPYPPSLQWGGIPREVS GALPRPGSIITFP 480
 QY 481 RDDRYWRLDQAKLTATTSGRWATELPMWGCWHAHSGSLF 520
 DB 481 RDDRYWRLDQAKLTATTSGRWATELPMWGCWHAHSGSLF 520

RESULT 2
 AAB74690
 ID AAB74690 standard; protein; 520 AA.

XX
 AC AAB74690;

XX
 DT 12-JUN-2001 (first entry)

DE Human protease and protease inhibitor PPIIM-23.

KM Human; protease; protease inhibitor; protease and protease inhibitor;
 KM PPIIM; identification; diagnosis; anti-human immunodeficiency virus; HIV;
 KM antidiabetic; immunostimulant; immunomodulator; antiinflammatory;
 KM antitumor; immunosuppressive; nephrotropic; antitumor; thyromimetic;

KM cytostatic; antibacterial; fungicide; protozoacide; antitubercular;
 KM antitubercular; antiparasitic; virucide; hepatotropic; gene therapy;
 KM autoimmune disorder; inflammatory disorder; AIDS; Dengue's syndrome;
 KM severe combined immunodeficiency disease; SCID; Chediak-Higashi syndrome;
 KM Cushing's disease; Addison's disease; autoimmune thyroiditis; gout;
 KM Crohn's disease; diabetes mellitus; Good pasture's syndrome; infection;
 KM Grave's disease; Hashimoto's thyroiditis; Sjogren's syndrome; cancer;
 KM Werner's syndrome; cell proliferative disorder; arteriosclerosis;
 KM atherosclerosis; cirrhosis; hepatitis; psoriasis.

XX Homo sapiens.

XX WO200110903-A2.

XX 15-FEB-2001.

XX 09-AUG-2000; 2000WO-US021078.

XX 09-AUG-1999; 99US-0147966P.

XX 21-OCT-1999; 99US-0160807P.

XX (INCY-) INCYTE GENOMICS INC.

XX Yue H, Lal P, Tang YT, Bandman O, Baughn MR, Azimzai Y, Lu DM;
 PI Yang J;

XX WPI; 2001-202760/20.

XX N-PSDB; AAF81736.

PT New protease (inhibitors) useful for diagnosis and treatment of
 PT autoimmune/inflammatory disorders such as acquired immunodeficiency
 PT syndrome, Cushing's disease, Addison's disease and cell proliferative
 PT disorders such as cancer.

XX Claim 1; Page 111-112; 134pp; English.

CC AAF8174 to AAF81740 encode the human proteases and protease inhibitors
 CC (PPIIMs) given in AAB74690 to AAB74694. The PPIIMs can have activities such
 CC as: anti-human immunodeficiency virus (HIV); antidiabetic; antitumor;
 CC immunostimulant; immunomodulator; antiinflammatory; immunosuppressive;
 CC nephrotropic; antitumor; thyromimetic; cytostatic; antibacterial;
 CC fungicide; protozoacide; antitubercular; antitubercular;
 CC virucide; antiparasitic; and hepatotropic. PPIIM polynucleotide and
 CC protein sequences can be used in the diagnosis, treatment and prevention
 CC of autoimmune/inflammatory disorders such as AIDS, Dengue's syndrome,
 CC severe combined immunodeficiency disease (SCID), Chediak-Higashi
 CC syndrome, Cushing's disease, Addison's disease, autoimmune thyroiditis,
 CC Crohn's disease, diabetes mellitus, Good pasture's syndrome, gout,
 CC Grave's disease, Hashimoto's thyroiditis, Sjogren's syndrome, Werner's
 CC syndrome, viral, bacterial, fungal, parasitic, protozoal, and helminthic
 CC infections and cell proliferative disorder such as arteriosclerosis,
 CC atherosclerosis, cirrhosis, hepatitis, psoriasis and cancer. PPIIM
 CC polynucleotide sequences can be used in somatic or germ line gene therapy
 CC and in diagnosis of diseases. They can also be used in generating
 CC hybridization probes useful in mapping the naturally occurring genomic
 CC sequences and in molecular biology techniques

XX Sequence 520 AA;

Query Match 87.2%; Score 2472; DB 4; Length 520;
 Best Local Similarity 88.9%; Pred. No. 46-218;
 Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MVARVGLLRALQLLMGHLDAQPAERGGOELRKEAEAFLEKYGYNLEQVPAPPTSTRS 60
 DB 1 MVARVGLLRALQLLMGHLDAQPAERGGOELRKEAEAFLEKYGYNLEQVPAPPTSTRS 60
 QY 61 DAIRAFQWYSQLPVSGVLDRAITRQMTPRCGVTDNTSYAAMERISDLFAHRRTKMRK 120
 DB 61 DAIRAFQWYSQLPVSGVLDRAITRQMTPRCGVTDNTSYAAMERISDLFAHRRTKMRK 120
 QY 121 KEPAQGNKWKYKQHLSTYLVNMPENHSRQFAPCAPPSSCGATSGRPSGRPOAPLIT 180
 DB 121 KEPAQGNKWKYKQHLSTYLVNMPENHSRQFAPCAPPSSCGATSGRPSGRPOAPLIT 180

PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 05-JAN-2000; 99WO-US031274.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 11-FEB-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005004.
 PR 03-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007277.
 PR 21-MAR-2000; 2000WO-US007332.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000WO-US009832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Flvaroff B, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
 XX
 DR WPI: 2001-408281/43.
 DR N-PSDB; AAS21315.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 XX breast, prostate, cervical.
 XX
 PS Claim 12; Fig 144; 813p; English.
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation of
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 CC
 XX Sequence 520 AA;
 SQ

Query Match 87.2%; Score 2472; DB 4; Length 520;
 Best Local Similarity 88.9%; Pred. No. 4e-218;
 Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MYARVGLLRALQQLMGLHLDQAPRGGQELRKAFAFLKRYGLYNQVPAKPTSTPS 60
 DB 1 MYARVGLLRALQQLMGLHLDQAPRGGQELRKAFAFLKRYGLYNQVPAKPTSTPS 60
 QY 61 DAIRAFQWVSQLPVSGVLDRAATLRQMTPRGCVTDYTNVYAAWAEISDLPARHTKMRK 120
 DB 61 DAIRAFQWVSQLPVSGVLDRAATLRQMTPRGCVTDYTNVYAAWAEISDLPARHTKMRK 120
 QY 121 KRFAQGNKWKYKQHLSTYLVNWPPEHLBSRGAPCAPSSCGATS---GRWS--SGRPQP 175
 DB 121 KRFAQGNKWKYKQHLSTYLVNWPPEHLBSRGAPCAPSSCGATS---GRWS--SGRPQP 175
 QY 176 QAPLTSGSPSS-----KGTTMGWAMPMLMQGAPWMTPTPLPRGGEAHFODDERWSLSRR 229
 DB 172 EAPAT--GPADIRLRLFFQGDHNDGLGNAFPGCGALHAFLPRGGEAHFODDERWSLSRR 229
 QY 230 RGRNLPVTVLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALLSWDPVLAQSLYKPLGG 289
 DB 230 RGRNLPVTVLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALLSWDPVLAQSLYKPLGG 289
 QY 290 SVAVOLPKLPTDEPETWDSYSPQGRREPQPKYCHSSPFAITYDRQOQLYIFKGSFWFE 349
 DB 290 SVAVOLPKLPTDEPETWDSYSPQGRREPQPKYCHSSPFAITYDRQOQLYIFKGSFWFE 349
 QY 350 VAADGNVSEPRPLQERWVGLPNNIEAAVSLNDGDFYFFKGRGCMFRPKPVMGLPOLC 409
 DB 350 VAADGNVSEPRPLQERWVGLPNNIEAAVSLNDGDFYFFKGRGCMFRPKPVMGLPOLC 409
 QY 410 RAGGLPRHPDPAALFPPPLRLILFKGARVYVLAARGQLQVEPYPRSLQMGWGIPEEVSQA 469
 DB 410 RAGGLPRHPDPAALFPPPLRLILFKGARVYVLAARGQLQVEPYPRSLQMGWGIPEEVSQA 469
 QY 470 LPRPDGSIIFPRDRYWRDLQATLQATTSGRWATELPMWGCWMAHNSGSLF 520
 DB 470 LPRPDGSIIFPRDRYWRDLQATLQATTSGRWATELPMWGCWMAHNSGSLF 520

RESULT 5

AAU79810 standard; protein; 520 AA.
 AAU79810;

02-JUL-2002 (first entry)

Novel matrix metalloproteinase 46798, long form.

Matrix metalloproteinase; MMP; 46798 long form; heart failure; tumour;
 extracellular matrix degradation; cardiovascular disease; metastasis;
 atherosclerosis; arthritis; nephritis; neurological disease; ischaemia;
 periodontal disease; skin ulceration; liver fibrosis; emphysema; trachea;
 fibrotic lung disease; bacterial infection; viral infection; psoriasis;
 wound healing; chronic injury; autoimmune disorder; angiogenesis;
 tissue invasion.

Homo sapiens.

WO200220739-A2.

14-MAR-2002.

10-SEP-2001; 2001WO-US028260.

08-SEP-2000; 2000US-0231136P.

(MILL-) MILLENNIUM PHARM INC.

Curtis RAJ;

DR WPI; 2002-351776/38.
DR N-PSDB; ABR48980.

PT New human matrix metalloproteinase and polymucleotides useful for
PT diagnosing and treating atherosclerosis, bacterial and viral infections,
PT wound healing, chronic injury, traumatic, ischemia and psoriasis.

XX PS Claim 9; Fig 1A-D; 133pp; English.

XX The invention describes a novel isolated human matrix metalloproteinase
CC (MMP) polypeptide (I) 46798, (I) and the polynucleotide encoding it (II)
CC are useful for evaluating the efficacy of a treatment of a disorder. (I)
CC is useful as novel diagnostic target and therapeutic agent for
CC prognosticating, diagnosing, preventing, inhibiting, alleviating or
CC curing MMP-related disorders, where (I) functions in normal tissues to
CC facilitate growth, repair, replacement or renewal of endothelial,
CC epithelial, and neuronal tissues, by remodeling or degrading
CC extracellular matrix through or into which new endothelial, epithelial,
CC or neuronal cells must move, grow or proliferate. Examples of the
CC disorders involving degradation of the extracellular matrix include
CC cardiovascular diseases e.g. heart failure and atherosclerosis,
CC arthritis, nephritis, neurological disease, periodontal disease, skin
CC ulceration, liver fibrosis, emphysema, fibrotic lung disease, bacterial
CC and viral infections, wound healing, chronic injury, acute disorder
CC (autoimmune disorder), traumatic, ischemia, psoriasis, aberrant
CC angiogenesis and tissue invasion and metastasis by tumour cells. This is
CC the amino acid sequence of the long form of the novel human matrix
CC metalloproteinase 46798 described in the invention

XX Sequence 520 AA;

Query Match 87.2%; Score 2472; DB 5; Length 520;

Best Local Similarity 88.9%; Pred. No. 4e-218;

Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

```

QY 1 MYARVGLLRLALQLLMGHLDAPARSGQELRKEAEFLKRYGYNQVPAPTSTPS 60
DB 1 MYARVGLLRLALQLLMGHLDAPARSGQELRKEAEFLKRYGYNQVPAPTSTPS 60
QY 61 DAIRAFQWVSQPVSGVLDRLATLRQMTBRGCVTDNNSVAAMERSDIPAHRTMRK 120
DB 61 DAIRAFQWVSQPVSGVLDRLATLRQMTBRGCVTDNNSVAAMERSDIPAHRTMRK 120
QY 121 KRFPAQGNKMYKQHLSTYRLVNPPEHLRSQFAPCAPSSCATS---QRMS--SGRPOP 175
DB 121 KRFPAQGNKMYKQHLSTYRLVNPPEHLRSQFAPCAPSSCATS---QRMS--SGRPOP 175
QY 176 QAPLTSGSPSS-----KSTTWGAMPMIAQAPWRTPLPRGGAHFDDERMSLSRR 229
DB 176 QAPLTSGSPSS-----KSTTWGAMPMIAQAPWRTPLPRGGAHFDDERMSLSRR 229
QY 230 RGRNLFVYLAHEGHTLGLTSPAPALMAFYKRLGRALLSMDVLAVALSYKCPPLG 289
DB 230 RGRNLFVYLAHEGHTLGLTSPAPALMAFYKRLGRALLSMDVLAVALSYKCPPLG 289
QY 290 SYAVOLPGKLFPTDPTWDSYSPQGRRPETQGPYCHSSFDATTVDRQOOLYFKGSHFE 349
DB 290 SYAVOLPGKLFPTDPTWDSYSPQGRRPETQGPYCHSSFDATTVDRQOOLYFKGSHFE 349
QY 350 VAADGVNSBRPLQERWGLPNIEAAVSLNDGDFYFKGGRGCRWFRGPKFVWGLPOLC 409
DB 350 VAADGVNSBRPLQERWGLPNIEAAVSLNDGDFYFKGGRGCRWFRGPKFVWGLPOLC 409
QY 410 RAGGILPRHEDALFPPRLRRLIFKGRYYVLARGLQVPEPYPSLQWGGIPREVSGA 469
DB 410 RAGGILPRHEDALFPPRLRRLIFKGRYYVLARGLQVPEPYPSLQWGGIPREVSGA 469
QY 470 LRPDGSIIFFRDDRWRLDQAKLQATTSGRWATELPMWGCWHAHNSGSLF 520
DB 470 LRPDGSIIFFRDDRWRLDQAKLQATTSGRWATELPMWGCWHAHNSGSLF 520

```

RESULT 6

ABG31460
ID ABG31460 standard; protein; 520 AA.

XX AC ABG31460;

XX DT 29-NOV-2002 (first entry)

XX DE Human matrix metalloproteinase (MMP) 46798 #2.

XX Human; matrix metalloproteinase; MMP 46798; cell proliferation disorder;
KW cell differentiation disorder; carcinoma; sarcoma; leukaemia;
KW breast cancer; lung cancer; neurological disorder; schizophrenia;
KW ischaemia; infarction; Parkinson's disease; Huntington's disease;
KW inflammatory disorder; Crohn's disease; immune disorder; arthritis;
KW diabetes mellitus; cardiovascular disorder; resectosis; tachycardia;
KW rheumatic heart disease; motility disorder; developmental disorder;
KW lung disorder; chronic bronchitis; pulmonary congestion; oedema;
KW blood disorder; blood clotting disorder; cytosolic; immunomodulator;
KW anti-inflammatory; cardiac; antiparkinsonian; nootropic; thrombolytic;
KW neuroprotective; antidiabetic; antirheumatic; antiarthritic; vasotropic;
KW enzyme.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Domain 39..225

XX FT Domain /label= Peptidase_M10_domain

XX FT Domain 328..371

XX FT Domain /label= Haemopexin-like_domain

XX FT Domain 373..416

XX FT Domain /label= Haemopexin-like_domain

XX FT Domain 418..464

XX FT Domain /label= Haemopexin-like_domain

XX FT Domain 466..510

XX FT Domain /label= Haemopexin-like_domain

XX PN WO20026670-A2.

XX PD 29-AUG-2002.

XX PP 16-JAN-2002; 2002WO-US001546.

XX PR 16-JAN-2001; 2001US-026252P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Curtis RAJ, Lora JM;

XX PT WPI; 2002-674955/72.

XX DR N-PSDB; ABR91096.

PT New human matrix metalloproteinase nucleic acid and polypeptide
PT molecules, designated 46798, useful for diagnosing, preventing or
PT treating cancers, ischemia, Parkinson's disease heart disease or edema.

XX Claim 17; Page 113-114; 117pp; English.

XX The present invention relates to the isolation of novel human matrix
CC metalloproteinases (MMP), designated 46798, and the polynucleotide
CC sequences encoding them. The MMP 46798 polypeptide and polynucleotide
CC sequences are useful for diagnosing, preventing, alleviating or treating
CC metalloproteinase-associated disorders such as cell proliferation and/or
CC differentiation disorders (e.g. carcinoma, sarcoma, leukaemia, breast
CC cancer, or lung cancer), neurological disorders (e.g. schizophrenia,
CC ischaemia, infarction, Parkinson's disease or Huntington's disease),
CC inflammatory disorders (e.g. Crohn's disease) or immune disorders (e.g.
CC diabetes mellitus or arthritis), cardiovascular disorders (e.g.
CC resectosis, tachycardia or rheumatic heart disease), motility disorders,
CC developmental disorders, lung disorders (e.g. chronic bronchitis,
CC pulmonary congestion or oedema), and blood/blood clotting disorders. The
CC present sequence represents human MMP 46798 #2

XX Sequence 520 AA;

Query Match 87.2%; Score 2472; DB 5; Length 520;
Best Local Similarity 88.9%; Pred. No. 4e-218;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MVAEGLLRALQILLMGLHDAOPAEFGGSELKEAEAFLEKGYLYNEQVPAKPTSTRFS 60
Db 1 MVAEGLLRALQILLMGLHDAOPAEFGGSELKEAEAFLEKGYLYNEQVPAKPTSTRFS 60
QY 61 DAIAFQWVSQLPVSGVLDRAITLQMTFRPGVDTNSYAAMERISDLFARHTMKRR 120
Db 61 DAIAFQWVSQLPVSGVLDRAITLQMTFRPGVDTNSYAAMERISDLFARHTMKRR 120
QY 121 KRFAKQGNKMYKQHLSTYRLVWMPHLSRQFGAPCAFPSSCGATSS--QWSS--SGRPOP 175
Db 121 KRFAKQGNKMYKQHLSTYRLVWMPHLSRQFGAPCAFPSSCGATSS--QWSS--SGRPOP 175
QY 176 QAPLTSSPSS-----KGTITMGWAMPILMAOGAPMPTPLPRGEAHFPODERMSLSRR 229
Db 172 EAPAT--GPADIRLTFPGQDHNGLGNAFPGGALAHAFPRGSAHFPODERMSLSRR 229
QY 230 RGRNLFPVLAHEIGHTLGLTHSPAPALMAPYKRLGRDALLSMDDVLAQSLYKPLGG 289
Db 230 RGRNLFPVLAHEIGHTLGLTHSPAPALMAPYKRLGRDALLSMDDVLAQSLYKPLGG 289
QY 290 SVAVOLPGKLTDFETWDSYSPQGRREPQKCHSSFDATVDRQOOLYFKGSHWE 349
Db 290 SVAVOLPGKLTDFETWDSYSPQGRREPQKCHSSFDATVDRQOOLYFKGSHWE 349
QY 350 VAADVNSEPRPQOERWVGIPNIEAAVSLNDGDFPFKGRGCRFRGPKVWGIPOLC 409
Db 350 VAADVNSEPRPQOERWVGIPNIEAAVSLNDGDFPFKGRGCRFRGPKVWGIPOLC 409
QY 410 RAGGLPRHPDALFFPPLRLILFKGARYYVLARGLQVEPYPPSLDQWGIPEEVSQA 469
Db 410 RAGGLPRHPDALFFPPLRLILFKGARYYVLARGLQVEPYPPSLDQWGIPEEVSQA 469
QY 470 LRPDGSIIFFRDRYWRLDQAKLQATTSGRWATELPMWGCWANSGLAF 520
Db 470 LRPDGSIIFFRDRYWRLDQAKLQATTSGRWATELPMWGCWANSGLAF 520

RESULT 7
ABOI7687
ID ABOI7687 standard; protein; 520 AA.
XX
AC ABOI7687;
XX
DT 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO4339.
XX
KW Human; secreted and transmembrane protein; PRO; anti-inflammatory;
KW antiarteriosclerotic; cardiant; anti-fertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003032156-A1.
XX
PD 13-FEB-2003.
XX
PF 06-MAY-2002; 2002US-00140474.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.

PR 14-JUL-1998; 98WO-US014552.
PR 26-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US0005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028851.
PR 02-DEC-1999; 99WO-US028854.
PR 16-DEC-1999; 99WO-US028855.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005064.
PR 02-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US007532.
PR 17-MAY-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US013705.
PR 30-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US014941.
PR 28-JUL-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US020710.
PR 23-AUG-2000; 2000WO-US022031.
PR 24-AUG-2000; 2000WO-US023522.
PR 08-NOV-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US030873.
PR 20-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.

PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00860342.
 PR 25-MAY-2001; 2001US-00866034.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001US-00872035.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001US-00919692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001US-00920116.
 PR 29-JUN-2001; 2001US-00921066.
 PR 09-JUL-2001; 2001US-00921735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927766.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX (GENTH) GENENTECH INC.
 PA Baker KP, Beteshti M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerlicien ME, Goddard A, Godowski PO, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2003-341980/32.
 DR N-PSDB; ACD23924.
 XX
 PT New secreted and transmembrane PRO nucleic acids, for treating
 PT inflammation, organ failure, atherosclerosis, cardiac injury,
 PT infertility, birth defects, premature aging, acquired immunodeficiency
 PT syndrome (AIDS), or cancer.
 XX
 PS Claim 12; Fig 144; 660pp; English.
 CC The invention describes an isolated nucleic acid (1) comprising, or which
 CC has 80 % sequence identity to, or the full-length coding sequence of, one
 CC of 275 nucleotide sequences, and which encodes a corresponding
 CC polypeptide selected from 275 amino acid sequences, where all sequences
 CC are given in the specification. The polypeptide encoded by (1) is used to
 CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
 CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
 CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
 CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
 CC the proliferation or differentiation of cells or gene expression.
 CC stimulate the release of proteoglycans, stimulate the release of cytokine
 CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
 CC to factor VIIa, or detect the presence of tumour in a mammal. The nucleic
 CC acid and polypeptide encoded by it, are useful for treating inflammatory
 CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
 CC birth defects, premature aging, acquired immunodeficiency syndrome
 CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
 CC hybridisation probes, in chromosome and gene mapping, and in generating
 CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
 CC diagnostic, biosensors or bioreactors. Both are useful in tissue typing.
 CC This is the amino acid sequence of a novel human secreted and
 CC transmembrane PRO polypeptide
 XX
 SO Sequence 520 AA;

Query Match 87.2%; Score 2472; DB 6; Length 520;
 Best Local Similarity 88.9%; Pred. No. 4e-218;
 Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MVARVGLLRALQLQLMGLHDAQPARGGQELRKEAEALFKYGYLNEQVPAAPSTSTRS 60
 DB 1 MVARVGLLRALQLQLMGLHDAQPARGGQELRKEAEALFKYGYLNEQVPAAPSTSTRS 60

QY 61 DAIRAFQWVSQLPVSGVLDRAFLRQMTSPRCQVTDNLSYAAMAEIRISDLFAHRTMKRK 120
 DB 61 DAIRAFQWVSQLPVSGVLDRAFLRQMTSPRCQVTDNLSYAAMAEIRISDLFAHRTMKRK 120
 QY 121 KEPAQGNKMYKQHLSTYLVNMPHURSRQFQCAPPSSCGATS--GRWG--SGRPOP 175
 DB 121 KEPAQGNKMYKQHLSTYLVNMPHURSRQFQCAPPSSCGATS--GRWG--SGRPOP 175
 QY 176 QAPLTSGSPSS-----KGTMTGWAMPMLAAGAPWRPFELPRRGAHFDQDERMSLSR 229
 DB 172 EAPAT--GPADIRLTFQGDHNDGLGNMFDFGALAHAFPRRGAHFDQDERMSLSR 229
 QY 220 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALISWDVLAQSLYKPLCG 289
 DB 220 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALISWDVLAQSLYKPLCG 289
 QY 230 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALISWDVLAQSLYKPLCG 289
 DB 230 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALISWDVLAQSLYKPLCG 289
 QY 290 SVAVOLPGKLPDPEFTWDSYSPQGRPETQGRKYCHSSFDATVDRQQQLYIFKSHFWE 349
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 QY 350 VAADNVSEPRPLQGRWGLPNTBAAVSLNDGDFYFPGKGRCMRFRGKPVWGLPOLC 409
 DB 350 VAADNVSEPRPLQGRWGLPNTBAAVSLNDGDFYFPGKGRCMRFRGKPVWGLPOLC 409
 QY 410 RAGGLPRHPDALFPPLRLILFKGARYYVLARGALQVEPYPSLQDMGSIPEEVSQA 469
 DB 410 RAGGLPRHPDALFPPLRLILFKGARYYVLARGALQVEPYPSLQDMGSIPEEVSQA 469
 QY 470 LRPDGSIIFFPDRIYWRIDQAKLQATTSGRVATELPMWGCWANSQSALF 520
 DB 470 LRPDGSIIFFPDRIYWRIDQAKLQATTSGRVATELPMWGCWANSQSALF 520

RESULT 8
 ABU80941
 ID ABU80941 strand1; protein; 520 AA.

XX ABU80941;

DT 23-JUN-2003 (first entry)

XX Human PRO polypeptide #72.

KW Human; PRO polypeptide; secreted and transmembrane protein;

KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;

KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;

KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;

KW hearing loss; coagulation disorder; stroke; heart attack; cardiatic;

KW antidiabetic; anorectic; vulnary; antirheumatic; osteopathic;

KW antirheumatic; auditory; cerebroprotective; angiogenic.

OS Homo sapiens.

PN US200304311-A1.

XX 02-JAN-2003.

PD 19-DEC-2001; 2001US-00028072.

PF 18-JUN-1997; 97US-0049911P.

PR 26-AUG-1997; 97US-0056974P.

PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059122P.

PR 18-SEP-1997; 97US-0059263P.

PR 19-SEP-1997; 97US-0059352P.

PR 19-SEP-1997; 97US-0059383P.

PR 24-SEP-1997; 97US-0062250P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062285P.

PR	17-OCT-1997;	97US-0062287P.
PR	17-OCT-1997;	97US-0063755P.
PR	24-OCT-1997;	97US-0062814P.
PR	24-OCT-1997;	97US-0062816P.
PR	24-OCT-1997;	97US-0063045P.
PR	24-OCT-1997;	97US-0063082P.
PR	24-OCT-1997;	97US-0063127P.
PR	27-OCT-1997;	97US-0063327P.
PR	27-OCT-1997;	97US-0063329P.
PR	26-OCT-1997;	97US-0063502P.
PR	26-OCT-1997;	97US-0063561P.
PR	29-OCT-1997;	97US-0063704P.
PR	29-OCT-1997;	97US-0063733P.
PR	29-OCT-1997;	97US-0063735P.
PR	29-OCT-1997;	97US-0063738P.
PR	03-NOV-1997;	97US-0064248P.
PR	07-NOV-1997;	97US-0064809P.
PR	12-NOV-1997;	97US-0065186P.
PR	17-NOV-1997;	97US-0065846P.
PR	21-NOV-1997;	97US-0066434P.
PR	24-NOV-1997;	97US-0066453P.
PR	24-NOV-1997;	97US-0066511P.
PR	11-DEC-1997;	97US-0066770P.
PR	11-DEC-1997;	97US-0069212P.
PR	11-DEC-1997;	97US-0069278P.
PR	16-DEC-1997;	97US-0069334P.
PR	23-JAN-1998;	98US-0072320P.
PR	04-FEB-1998;	98US-0073612P.
PR	09-FEB-1998;	98US-0074086P.
PR	09-FEB-1998;	98US-0074092P.
PR	12-MAR-1998;	98US-0077791P.
PR	20-MAR-1998;	98US-0078910P.
PR	25-MAR-1998;	98US-0079294P.
PR	27-MAR-1998;	98US-0079663P.
PR	31-MAR-1998;	98US-0079728P.
PR	12-JUN-1998;	98US-0080165P.
PR	14-JUL-1998;	98WO-US012456.
PR	28-AUG-1998;	98WO-US014552.
PR	10-SEP-1998;	98WO-US017888.
PR	14-SEP-1998;	98WO-US018824.
PR	14-SEP-1998;	98WO-US019093.
PR	14-SEP-1998;	98WO-US019094.
PR	16-SEP-1998;	98WO-US019177.
PR	17-SEP-1998;	98WO-US019310.
PR	07-OCT-1998;	98WO-US019437.
PR	29-OCT-1998;	98WO-US021141.
PR	29-OCT-1998;	98WO-US022991.
PR	20-NOV-1998;	98WO-US022992.
PR	01-DEC-1998;	98WO-US024855.
PR	05-JAN-1999;	98WO-US025108.
PR	08-MAR-1999;	99WO-US000106.
PR	10-MAR-1999;	99WO-US005028.
PR	20-APR-1999;	99WO-US005190.
PR	14-MAY-1999;	99WO-US008615.
PR	02-JUN-1999;	99WO-US010733.
PR	01-SEP-1999;	99WO-US012252.
PR	08-SEP-1999;	99WO-US020111.
PR	13-SEP-1999;	99WO-US020594.
PR	15-SEP-1999;	99WO-US020944.
PR	15-SEP-1999;	99WO-US021090.
PR	05-OCT-1999;	99WO-US021547.
PR	29-NOV-1999;	99WO-US023089.
PR	30-NOV-1999;	99WO-US028214.
PR	30-NOV-1999;	99WO-US028313.
PR	01-DEC-1999;	99WO-US028409.
PR	01-DEC-1999;	99WO-US028301.
PR	02-DEC-1999;	99WO-US028634.
PR	02-DEC-1999;	99WO-US028564.
PR	02-DEC-1999;	99WO-US028565.
PR	16-DEC-1999;	99WO-US030095.
PR	20-DEC-1999;	99WO-US030911.
PR	17-OCT-1997;	97US-0062287P.
PR	17-OCT-1997;	97US-0063755P.
PR	24-OCT-1997;	97US-0062814P.
PR	24-OCT-1997;	97US-0062816P.
PR	24-OCT-1997;	97US-0063045P.
PR	24-OCT-1997;	97US-0063082P.
PR	24-OCT-1997;	97US-0063127P.
PR	27-OCT-1997;	97US-0063327P.
PR	27-OCT-1997;	97US-0063329P.
PR	26-OCT-1997;	97US-0063502P.
PR	26-OCT-1997;	97US-0063561P.
PR	29-OCT-1997;	97US-0063704P.
PR	29-OCT-1997;	97US-0063733P.
PR	29-OCT-1997;	97US-0063735P.
PR	29-OCT-1997;	97US-0063738P.
PR	03-NOV-1997;	97US-0064248P.
PR	07-NOV-1997;	97US-0064809P.
PR	12-NOV-1997;	97US-0065186P.
PR	17-NOV-1997;	97US-0065846P.
PR	21-NOV-1997;	97US-0066434P.
PR	24-NOV-1997;	97US-0066453P.
PR	24-NOV-1997;	97US-0066511P.
PR	11-DEC-1997;	97US-0066770P.
PR	11-DEC-1997;	97US-0069212P.
PR	11-DEC-1997;	97US-0069278P.
PR	16	

Db 290 SVAVLPGKLTDFDTMTDYSFQGRRPETQGPKYCHSSFDALTVDROOQLYFKGSHWE 349
Qy 350 VAADGNVESEPRPLQGRWVGLPNNIEAAVSLNDGDFYFFPKGRCWRFRGPKFVWGLPOLC 409
Db 350 VAADGNVESEPRPLQGRWVGLPNNIEAAVSLNDGDFYFFPKGRCWRFRGPKFVWGLPOLC 409
Qy 410 RAGGLPRHPDALFPPLRLRLILFKGARYVYLARGGLQVEPYPRSLQDMGIPREVSQA 469
Db 410 RAGGLPRHPDALFPPLRLRLILFKGARYVYLARGGLQVEPYPRSLQDMGIPREVSQA 469
Qy 470 LPRPGSIIFFRDDRYWRDLQAKQATTSGRWATELPMWGMHANSGLF 520
Db 470 LPRPGSIIFFRDDRYWRDLQAKQATTSGRWATELPMWGMHANSGLF 520

RESULT 9
ABU66641
ID ABU66641 standard; protein; 520 AA.
XX
AC ABU66641;
XX
DT 23-MAY-2003 (first entry)
XX
DE Human PRO polypeptide #72.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
XX
PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-00143114.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028651.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030939.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUN-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00924796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
(GENTH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
PI Smith V, Stewart RA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
DR WPI; 2003-332040/31.
DR N-PSDB; ACN03674.
XX

PT New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.

XX Claim 12; Fig 144; 660pp; English.

XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC stimulating the release of tumor necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumors. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridization probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. AB06570-AB06684 represent the
CC human PRO polypeptides of the invention. Note: The sequence data for this
CC patent was obtained in electronic format directly from the USPTO web site
CC at seqdata.uspto.gov/psipdsidentry.html

XX Sequence 520 AA;

Query Match 87.2%; Score 2472; DB 6; Length 520;
Best Local Similarity 88.9%; Pred. No. 4e-218;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MVARVGLRLALQLLMGLHLDAPRGQELRKAEAELEKYGLNVPAPSTPS 60
DB 1 MVARVGLRLALQLLMGLHLDAPRGQELRKAEAELEKYGLNVPAPSTPS 60
QY 61 DAIRAFQWVSQLPVSGVLDRAITRQWTRPCGVTDTNSYAAMERISDLFAHRTQMRK 120
DB 61 DAIRAFQWVSQLPVSGVLDRAITRQWTRPCGVTDTNSYAAMERISDLFAHRTQMRK 120
QY 121 KRFAQGNKWKYKQHLSTYLVNMPHILRSQFAPCAPSSCCANS--GRSQP 175
DB 121 KRFAQGNKWKYKQHLSTYLVNMPHILRSQFAPCAPSSCCANS--GRSQP 175
QY 176 QAPLTSGSSPSS-----KQTTMGWAMFLMAQGAFWRPPLPRGEAFHDDERSLSRR 229
DB 172 EAPAT--GPADIRLRLFFQGDHNDGIGNAPDPGAGALAAFLPRGEAFHDDERSLSRR 229
QY 230 RGRNLFVTLAHEIGHTLGLTHSPAPRALMAPYKRLGSDALLSMDVLAVALGKPLGG 289
DB 230 RGRNLFVTLAHEIGHTLGLTHSPAPRALMAPYKRLGSDALLSMDVLAVALGKPLGG 289
QY 290 SVAVOLPEKLFPTDEFTWVSROGRPRPTQPKYCHSFDALITVDROQLYIFGSHFWE 349
DB 290 SVAVOLPEKLFPTDEFTWVSROGRPRPTQPKYCHSFDALITVDROQLYIFGSHFWE 349
QY 350 VAADGNVSEPRPLQERWGLPNNIEAAVSLNDGDFYFKGRCMRFRGPKVWGLPOLC 409
DB 350 VAADGNVSEPRPLQERWGLPNNIEAAVSLNDGDFYFKGRCMRFRGPKVWGLPOLC 409
QY 410 RAGGLPRPDAALFPPLRLRLIFKGAARYVLARGLQVEBYPRSLQDWGGLPEEVSQA 469
DB 410 RAGGLPRPDAALFPPLRLRLIFKGAARYVLARGLQVEBYPRSLQDWGGLPEEVSQA 469
QY 470 LPRPDGSIIFPRDRRYMLDQAKLQATTSGWAMELPMWGMWANSALF 520
DB 470 LPRPDGSIIFPRDRRYMLDQAKLQATTSGWAMELPMWGMWANSALF 520

RESULT 10
ABUS9722
ID ABUS9722 standard; protein; 520 AA.
XX
AC ABUS9722;

XX 13-MAY-2003 (first entry)
DT
XX

DE Novel secreted and transmembrane protein PRO4339.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.

OS Homo sapiens.

XX US2003017563-A1.

XX 23-JAN-2003.

XX 07-MAY-2002; 2002US-00140808.

XX 31-MAR-1997;

XX 12-JUN-1998;

XX 14-JUL-1998;

XX 28-AUG-1998;

XX 10-SEP-1998;

XX 14-SEP-1998;

XX 14-SEP-1998;

XX 14-SEP-1998;

XX 16-SEP-1998;

XX 17-SEP-1998;

XX 07-OCT-1998;

XX 29-OCT-1998;

XX 29-OCT-1998;

XX 20-NOV-1998;

XX 01-DEC-1998;

XX 05-JAN-1999;

XX 08-MAR-1999;

XX 10-MAR-1999;

XX 20-APR-1999;

XX 14-MAY-1999;

XX 02-JUN-1999;

XX 01-SEP-1999;

XX 08-SEP-1999;

XX 13-SEP-1999;

XX 15-SEP-1999;

XX 15-SEP-1999;

XX 05-OCT-1999;

XX 23-NOV-1999;

XX 30-NOV-1999;

XX 30-NOV-1999;

XX 01-DEC-1999;

XX 01-DEC-1999;

XX 01-DEC-1999;

XX 02-DEC-1999;

XX 02-DEC-1999;

XX 16-DEC-1999;

XX 20-DEC-1999;

XX 22-DEC-1999;

XX 30-DEC-1999;

XX 05-JAN-2000;

XX 06-JAN-2000;

XX 11-FEB-2000;

XX 18-FEB-2000;

XX 22-FEB-2000;

XX 24-FEB-2000;

24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001US-00908827.
PR 18-JUL-2001; 2001WO-US021735.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Betensin M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI: 2003-148338/14.
DR N-PSDB; ABX89212.
XX
XX Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.
XX
XX Claim 12; Fig 144; 659pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO132 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,

CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumors. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184 and PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetic forms or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1392 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
XX Sequence 520 AA;

Query Match 87.2%; Score 2472; DB 6; Length 520;
Best Local Similarity 88.9%; Pred. No. 48-218;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MYARVGLLRALQILIMKHLNQPARGGQGEIRKAEAFLEKYGLINEVPAPPISTRS 60
DB 1 MYARVGLLRALQILIMKHLNQPARGGQGEIRKAEAFLEKYGLINEVPAPPISTRS 60
QY 61 DAIRAFQWVSQLPVSGVDRLATLRQMTPRCGVDTNLSAAAEIRISDFAPHRTRMRK 120
DB 61 DAIRAFQWVSQLPVSGVDRLATLRQMTPRCGVDTNLSAAAEIRISDFAPHRTRMRK 120
QY 121 KRFAQGNKMYKQHLSTYRLVNPPEHLRSQFAPCAPSSCGATS---QRWS--SGRPOP 175
DB 121 KRFAQGNKMYKQHLSTYRLVNPPEHL-----PEPRVGAVVAAPQLMNVSLTEFM 171
QY 176 QAPLTSGSPSS-----KDTTGMAMPMLMAQAPWRTPFLPRGSAHFDDQERMSLSRR 229
DB 172 EAPAT--GPADIRLTFPQGDHNDGIGNAFDGPGALANAFPLRRGEAHFDQERMSLSRR 229
QY 230 RGRNLFVYLAHRIHTGLGTHSPAPRALMAPYKRLGSRALLSMQDYLAVQSLYKGPRLGG 289
DB 230 RGRNLFVYLAHRIHTGLGTHSPAPRALMAPYKRLGSRALLSMQDYLAVQSLYKGPRLGG 289
QY 290 SVAVOLPGKLFYDFETWDSYSPQGRRPETQGRKCHSFPDAITVDROOQLYFKGSHFWE 349
DB 290 SVAVOLPGKLFYDFETWDSYSPQGRRPETQGRKCHSFPDAITVDROOQLYFKGSHFWE 349
QY 350 VAADGNVSEPRPLQGRWGLPNIEAVALSNDGDFYFFKGGRGCRFRGPKRVWGIPLQIC 409
DB 350 VAADGNVSEPRPLQGRWGLPNIEAVALSNDGDFYFFKGGRGCRFRGPKRVWGIPLQIC 409
QY 410 RAGGLPRHPDALLFPPLRLTLFGARYYVLARGLQVEPRYPSLDMWGGIPREVSGA 469
DB 410 RAGGLPRHPDALLFPPLRLTLFGARYYVLARGLQVEPRYPSLDMWGGIPREVSGA 469
QY 470 LPRPGSIIFPRDDRYWRLDQAKLQATTSGRWATELPMWGCNHAHSGSALF 520
DB 470 LPRPGSIIFPRDDRYWRLDQAKLQATTSGRWATELPMWGCNHAHSGSALF 520

RESULT 11
ABO24912
ID ABO24912 standard; protein; 520 AA.
XX
XX ABO24912;
AC
XX
XX 05-SBP-2003 (first entry)
DT

XX Human secreted/transmembrane protein (PRO) #72.
 DE
 XX
 KW Human; PRO; secreted protein; transmembrane protein; tumour; cytostatic;
 KW gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;
 KW proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;
 KW BMC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell;
 KW chondrocyte cell proliferation; chondrocyte cell differentiation;
 KW pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;
 KW endothelial cell; A-peptide; factor VIIA.
 KW
 OS Homo sapiens.
 XX
 XX US2003036179-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 10-MAY-2002; 2002US-00142431.
 XX
 XX 31-MAR-1997; 97WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023069.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 16-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 22-DEC-1999; 99WO-US030720.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.

PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006650.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 05-JUN-2001; 2001WO-US017800.
 PR 14-JUN-2001; 2001US-00874503.
 PR 19-JUN-2001; 2001US-00882536.
 PR 20-JUN-2001; 2001US-00886342.
 PR 21-JUN-2001; 2001WO-US019692.
 PR 22-JUN-2001; 2001US-00887879.
 PR 29-JUN-2001; 2001WO-US020116.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX
 XX (GETH) GENENTECH INC.
 PA
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
 PI Gerritsen WE, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z,
 XX WPI; 2003-466355/44.
 DR N-PSDB; ACD41866.
 DR
 XX
 PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO114 or
 PT PRO4978, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 PS
 PS Claim 12, Fig 144; 659pp; English.
 XX
 XX The invention relates to an isolated nucleic acid comprising at least 80%
 CC sequence identity to a PRO (secreted and transmembrane protein) cDNA
 CC comprising a nucleic acid (a) encoding a PRO polypeptide, or its
 CC extracellular domain (with or without its associated signal peptide),
 CC which comprises any of the 275 120-850 residue amino acid sequences,
 CC given in the specification; (b) comprising any of the 275 300-3500
 CC nucleotide sequences, given in the specification; or (c) comprising the
 CC full-length coding sequence of the nucleotide sequences given in the
 CC specification, or of the DNA deposited under any of the American Type
 CC Culture Collection (ATCC) Accession Numbers listed in the specification.
 CC Also included are a vector comprising the novel nucleic acid, a host cell
 CC comprising the vector, producing a PRO polypeptide, the isolated PRO

polypeptides detailed above, a chimaeric molecule comprising the PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO antibody, detecting a PRO polypeptide in a sample suspected of containing the PRO polypeptide, linking a bioactive molecule to a cell expressing a PRO polypeptide, modulating at least one biological activity of a cell expressing a PRO polypeptide, stimulating the release of tumour necrosis factor- α (TNF- α) from human blood, (or proteoglycans from cartilage or cytokine from peripheral blood mononuclear cells (PBMC)), modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, stimulating the proliferation or differentiation of chondrocyte cells (or proliferation of or gene expression in pericyte cells), stimulating the proliferation of inner ear utricular supporting cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the binding of A-peptide to factor VIIa, or differentiation of adipocyte cells, detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences given in the specification. The polynucleotide is useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptide or the antibody is used in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as tumours, and in various diagnostic assays. The present sequence represents a PRO polypeptide

Sequence 520 AA:

Query Match 87.2%; Score 2472; DB 6; Length 520;
Best Local Similarity 88.9%; Pred. No. 4e-218;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

1 MVARVGLLRALQLIMGHLDAPARGGELKKEALELEKGYINEQVPAPISTRS 60
1 MVARVGLLRALQLIMGHLDAPARGGELKKEALELEKGYINEQVPAPISTRS 60
61 DAIRAFQWYSQLPVSGVLRATLRQMTTRPCGVTDNSTAAAMERISDFAHRTMRK 120
61 DAIRAFQWYSQLPVSGVLRATLRQMTTRPCGVTDNSTAAAMERISDFAHRTMRK 120
121 KRFAGQGNKMYKQHLSTYLVNMPHLSRQFGAPCAPSSCGATS--GRWS--SGRPOP 175
121 KRFAGQGNKMYKQHLSTYLVNMPHLSRQFGAPCAPSSCGATS--GRWS--SGRPOP 175
176 CAPPLTSGSSSS-----KSTTTMGAMAPLMAGAPKPTFPLPRRGAHFDODBRNSLSRR 229
176 CAPPLTSGSSSS-----KSTTTMGAMAPLMAGAPKPTFPLPRRGAHFDODBRNSLSRR 229
172 EAPAT--GPADIRLTFFQGDNDGNGAFDGGGALAHAFLLPRRGAHFDODBRNSLSRR 229
172 EAPAT--GPADIRLTFFQGDNDGNGAFDGGGALAHAFLLPRRGAHFDODBRNSLSRR 229
230 RGRNLFVVAHIEIGHTLSTHPAPRALMAPYKRLGRDALLSMDVLAVQSLYGRKLG 289
230 RGRNLFVVAHIEIGHTLSTHPAPRALMAPYKRLGRDALLSMDVLAVQSLYGRKLG 289
230 RGRNLFVVAHIEIGHTLSTHPAPRALMAPYKRLGRDALLSMDVLAVQSLYGRKLG 289
230 RGRNLFVVAHIEIGHTLSTHPAPRALMAPYKRLGRDALLSMDVLAVQSLYGRKLG 289
290 SVAVALPGKLTFTDFTWDSYSPQGRRPETQGPXYCHSSFDATTVDRQQLYTFKSGHFE 349
290 SVAVALPGKLTFTDFTWDSYSPQGRRPETQGPXYCHSSFDATTVDRQQLYTFKSGHFE 349
290 SVAVALPGKLTFTDFTWDSYSPQGRRPETQGPXYCHSSFDATTVDRQQLYTFKSGHFE 349
290 SVAVALPGKLTFTDFTWDSYSPQGRRPETQGPXYCHSSFDATTVDRQQLYTFKSGHFE 349
350 VAADGNVSEPRPLQGRWGLPNINIAAVALNDGDFYFFKGRGCMFRGPKFVWGIPQLC 409
350 VAADGNVSEPRPLQGRWGLPNINIAAVALNDGDFYFFKGRGCMFRGPKFVWGIPQLC 409
350 VAADGNVSEPRPLQGRWGLPNINIAAVALNDGDFYFFKGRGCMFRGPKFVWGIPQLC 409
350 VAADGNVSEPRPLQGRWGLPNINIAAVALNDGDFYFFKGRGCMFRGPKFVWGIPQLC 409
410 RAGGLPRHDDALFPPLRLTLFGARVYVLAAGSLQVEPYPPSLQDMGIPREVSQA 469
410 RAGGLPRHDDALFPPLRLTLFGARVYVLAAGSLQVEPYPPSLQDMGIPREVSQA 469
410 RAGGLPRHDDALFPPLRLTLFGARVYVLAAGSLQVEPYPPSLQDMGIPREVSQA 469
410 RAGGLPRHDDALFPPLRLTLFGARVYVLAAGSLQVEPYPPSLQDMGIPREVSQA 469
470 LPRPGSIIFFRDDRWRDLQAKLQATTSGRWATELPMWGCWHAHNSGSLF 520
470 LPRPGSIIFFRDDRWRDLQAKLQATTSGRWATELPMWGCWHAHNSGSLF 520
470 LPRPGSIIFFRDDRWRDLQAKLQATTSGRWATELPMWGCWHAHNSGSLF 520
470 LPRPGSIIFFRDDRWRDLQAKLQATTSGRWATELPMWGCWHAHNSGSLF 520

RESULT 12
ABU66917

ID ABU66917 standard; protein; 520 AA.
XX
AC ABU66917;
XX
DT 27-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane, PRO, protein SEQ ID 144.
XX
KW Human; secreted protein; transmembrane protein; PRO;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defects; premature aging; AIDS; biosensor;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW bioreactor; tumour.
XX
OS Homo sapiens.
XX
PN US2003032155-A1.
XX
PD 13-FEB-2003.
XX
PF 03-MAY-2002; 2002US-00137865.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US003365.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000MO-US005746.
PR 02-MAR-2000; 2000MO-US005841.
PR 10-MAR-2000; 2000MO-US006319.
PR 15-MAR-2000; 2000MO-US006884.
PR 20-MAR-2000; 2000MO-US007377.
PR 21-MAR-2000; 2000MO-US007533.
PR 30-MAR-2000; 2000MO-US008439.
PR 17-MAY-2000; 2000MO-US011705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 28-JUN-2000; 2000MO-US020710.
PR 11-AUG-2000; 2000MO-US020731.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023328.
PR 08-NOV-2000; 2000MO-US030952.
PR 10-NOV-2000; 2000MO-US030873.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000MO-US034725.
PR 20-DEC-2000; 2000MO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001MO-US006520.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00860028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001MO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001MO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001MO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001MO-US020116.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI: 2003-331925/31.
DR N-PSDB; ACA04095.
XX
XX New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
XX Claim 12; Fig 144; 659pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid further
CC comprises the full-length coding sequence of the DNA deposited under
CC American Type Culture Collection (ATCC) accession number in a list given
CC in the specification. Also included are vectors and host cells for
CC producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO

CC extracellular domains and mature sequences, methods of detecting PRO
CC proteins, methods for stimulating the release of TNF-alpha (tumour
CC necrosis factor alpha) from human blood, (and the proliferation of
CC differentiation of chondrocyte cells, the proliferation of, or gene
CC expression in pericyte cells, the release of proteoglycans from
CC cartilage, proliferation of inner ear utricular supporting cells, the
CC proliferation of T-lymphocyte cells, the release of a cytokine from
CC peripheral blood mononuclear cells (PBMC), or the proliferation of
CC endothelial cells), a method for modulating the uptake of glucose or free
CC fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the
CC binding of A-peptide to factor VIIA, or the differentiation of adipocyte
CC cells, a method for detecting the presence of a tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The nucleic acids and polypeptides are useful for treating
CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
CC infertility, birth defects, premature aging, AIDS (acquired
CC immunodeficiency syndrome), cancer, or diabetic complications. The
CC nucleic acids are useful as hybridisation probes, in chromosome and gene
CC mapping, and in generating antisense RNA or DNA. The polypeptides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both
CC are useful in tissue typing. The present sequence represents a PRO
CC protein of the invention
SQ
Sequence 520 AA;
Query Match 87.2%; Score 2472; DB 6; Length 520;
Best Local Similarity 88.9%; Pred. No. 4e-218;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;
QY 1 MVARVGLLRALQLLLGHLDAQPAERGGQDLREAEAEFLKYGYLNEOVKAPTSTFS 60
DB 1 MVARVGLLRALQLLLGHLDAQPAERGGQDLREAEAEFLKYGYLNEOVKAPTSTFS 60
QY 61 DAIRAFQWVSQLPVSGVLDRAATLROMTPRCGVDTNVSYAMARISDLPRRHTKRRK 120
DB 61 DAIRAFQWVSQLPVSGVLDRAATLROMTPRCGVDTNVSYAMARISDLPRRHTKRRK 120
QY 121 KRFAQGNKKYKQHLSTRLVNWPEHLRSRQFACAPSSCGATSS---QWSS--SGRPQP 175
DB 121 KRFAQGNKKYKQHLSTRLVNWPEHLRSRQFACAPSSCGATSS---QWSS--SGRPQP 175
QY 176 QAPITSSPSS-----KGTITGWMAPLMAQCAPWTPPLPRRGEAHPQDERWSLSRR 229
DB 176 QAPITSSPSS-----KGTITGWMAPLMAQCAPWTPPLPRRGEAHPQDERWSLSRR 229
QY 172 EAPAT--GPADIRLTFEGDNDLGNAPDGGALAAFLPRRGEAHPQDERWSLSRR 229
DB 172 EAPAT--GPADIRLTFEGDNDLGNAPDGGALAAFLPRRGEAHPQDERWSLSRR 229
QY 230 RGRNLFVYLAEHIGHTGLTHSPAPRALMAPYKRLGRDALLSMDVLAQVSLYGRPLGG 289
DB 230 RGRNLFVYLAEHIGHTGLTHSPAPRALMAPYKRLGRDALLSMDVLAQVSLYGRPLGG 289
QY 230 RGRNLFVYLAEHIGHTGLTHSPAPRALMAPYKRLGRDALLSMDVLAQVSLYGRPLGG 289
DB 230 RGRNLFVYLAEHIGHTGLTHSPAPRALMAPYKRLGRDALLSMDVLAQVSLYGRPLGG 289
QY 290 SVAVOLPGKLFDTDETWDYSPOGRREPOTGPKYCHSSFDAITVDRQOQLYIFKSHFWE 349
DB 290 SVAVOLPGKLFDTDETWDYSPOGRREPOTGPKYCHSSFDAITVDRQOQLYIFKSHFWE 349
QY 290 SVAVOLPGKLFDTDETWDYSPOGRREPOTGPKYCHSSFDAITVDRQOQLYIFKSHFWE 349
DB 290 SVAVOLPGKLFDTDETWDYSPOGRREPOTGPKYCHSSFDAITVDRQOQLYIFKSHFWE 349
QY 350 VAADGNVSEPRPQERWVGLPPIIEAAVSLNDGDFYFFKGRGCMFRGKPGWGLPQLC 409
DB 350 VAADGNVSEPRPQERWVGLPPIIEAAVSLNDGDFYFFKGRGCMFRGKPGWGLPQLC 409
QY 410 RAGGLPRHPALAFPPRLRLILFKGARVYVLAARGGLQVPEYPRSLQDQGGIPEEVSQA 469
DB 410 RAGGLPRHPALAFPPRLRLILFKGARVYVLAARGGLQVPEYPRSLQDQGGIPEEVSQA 469
QY 410 RAGGLPRHPALAFPPRLRLILFKGARVYVLAARGGLQVPEYPRSLQDQGGIPEEVSQA 469
DB 410 RAGGLPRHPALAFPPRLRLILFKGARVYVLAARGGLQVPEYPRSLQDQGGIPEEVSQA 469
QY 470 LPRPDGSIIFRDRRYWRLDQAKLQATTSGRWATLPMWGMCHANSQSALF 520
DB 470 LPRPDGSIIFRDRRYWRLDQAKLQATTSGRWATLPMWGMCHANSQSALF 520
QY 470 LPRPDGSIIFRDRRYWRLDQAKLQATTSGRWATLPMWGMCHANSQSALF 520
DB 470 LPRPDGSIIFRDRRYWRLDQAKLQATTSGRWATLPMWGMCHANSQSALF 520
RESULT 13
ADA45663
ID ADA45663 standard; protein; 520 AA.
XX
AC ADA45663;
XX
DT 20-NOV-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO4339.
DE Human; secreted and transmembrane protein; PRO;
XX Tumor necrosis factor alpha release; TNF-alpha release;
KW Glucose uptake modulator; PFA uptake modulator;
KW cell proliferation stimulator; cell differentiation stimulator;
KW cell differentiation inhibitor; cytokine release stimulator; tumor;
KW lung tumor; colon tumor; breast tumor; prostate tumor; rectal tumor;
KW cervical tumor; liver tumor; chromosome mapping; gene mapping;
KW gene therapy; chromosome identification; chromosome marker.
XX Homo sapiens.
OS
XX
XX US2003022328-A1.
PN
XX
XX 30-JAN-2003.
PD
XX
XX 16-APR-2002; 2002US-00123904.
XX
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 16-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022992.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 05-OCT-1999; 99WO-US021547.
PR 29-NOV-1999; 99WO-US023089.
PR 30-NOV-1999; 99WO-US028214.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 22-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 05-JAN-2000; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 18-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.

PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001US-00870992.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

XX (GENTH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Flyvareff E, Gao W;
PI Gerltsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tuma D, Watanabe CK, Wood WJ, Zhang Z;
XX WPI; 2003-584997/55.
XX N-PSDB; ADA45662.
XX
XX Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
XX Claim 12; Fig 144; 659p; English.
XX
XX The invention describes 305 nucleic acids encoding PRO (secreted and
CC transmembrane) polypeptides (I). (I) is useful for stimulating the
CC release of TNF-alpha from human blood, for modulating the uptake of
CC glucose or PFA by skeletal muscle cells or adipocyte cells, for
CC stimulating the proliferation or differentiation of chondrocyte cells,
CC for stimulating the proliferation of or gene expression in pericyte
CC cells, for stimulating the release of proteoglycans from cartilage, for
CC stimulating the proliferation of inner ear utricular supporting cells,
CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
CC the release of a cytokine from PBMC cells, for inhibiting the binding of
CC A-peptide to factor VIIa, for inhibiting the differentiation of adipocyte

CC cells, for stimulating proliferation of endothelial cells, for detecting
CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
CC prostate, rectal, cervical or liver tumour. The oligonucleotide probe
CC are useful for isolating genomic and cDNA nucleotide sequences or
CC antisense probes. (i) is also useful as therapeutic agent. PRO is useful
CC in assays to identify other proteins or molecules involved in binding
CC interaction. A polynucleotide (ii) encoding (i) is useful in chromosome
CC and gene mapping. In generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptide, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, in gene therapy, for
CC chromosome identification, as chromosome marker, and for generating
CC probes. An anti-(i)-antibody is useful in diagnostic assays for PRO, e.g.
CC detecting its expression in specific cells, tissues or serum, and for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. (i) and (ii) are useful for tissue typing. This is the amino
CC acid sequence of a novel human secreted and transmembrane PRO
CC polypeptide.
XX

SQ Sequence 520 AA;

Query Match 87.2%; Score 2472; DB 6; Length 520;
Best Local Similarity 88.9%; Pred. No. 4e-218;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MVARVGLLRALQLLMGHIDAPARGGGELAKAEAFLEKGYLANEQVPAPTSTRFS 60
DB 1 MVARVGLLRALQLLMGHIDAPARGGGELAKAEAFLEKGYLANEQVPAPTSTRFS 60
QY 61 DAIRAFQWWSQLPVSGLDRATLRQMTPRCGVTDNSYAAMERISDFARHRTKMRX 120
DB 61 DAIRAFQWWSQLPVSGLDRATLRQMTPRCGVTDNSYAAMERISDFARHRTKMRX 120
QY 121 KPRFQGNKMYKQHSYRLVNMPEHRSQFGAPCAPSSCGATS--SGRPOP 175
DB 121 KPRFQGNKMYKQHSYRLVNMPEHRSQFGAPCAPSSCGATS--SGRPOP 175
QY 176 QAPLTSGPS-----KGTTWGMAMPMAQGAAPRTPLPRGEAHFDDEKSLRR 229
DB 176 QAPLTSGPS-----KGTTWGMAMPMAQGAAPRTPLPRGEAHFDDEKSLRR 229
QY 172 EAPAT--GPADIRLTFPGQDNDHDLGNADGPGALANAFPRGEAHFDDEKSLRR 229
DB 172 EAPAT--GPADIRLTFPGQDNDHDLGNADGPGALANAFPRGEAHFDDEKSLRR 229
QY 230 RGRNLFVYLAHEIGTGLTTHSPAPRALMAPYKSLGRDALSMQDVAVOSLYGKPIG 289
DB 230 RGRNLFVYLAHEIGTGLTTHSPAPRALMAPYKSLGRDALSMQDVAVOSLYGKPIG 289
QY 230 RGRNLFVYLAHEIGTGLTTHSPAPRALMAPYKSLGRDALSMQDVAVOSLYGKPIG 289
DB 230 RGRNLFVYLAHEIGTGLTTHSPAPRALMAPYKSLGRDALSMQDVAVOSLYGKPIG 289
QY 290 SVAVOLPGKLTDFDEFTWMSYSPQGRRPETQGGKCHSSFDATYDRQQLYIFGSHFE 349
DB 290 SVAVOLPGKLTDFDEFTWMSYSPQGRRPETQGGKCHSSFDATYDRQQLYIFGSHFE 349
QY 350 VAADGNVSEPRPLQGRWVGLPENIEAAVSLNDGDFYFFKGGRCMRPRGKPVWGLPOLC 409
DB 350 VAADGNVSEPRPLQGRWVGLPENIEAAVSLNDGDFYFFKGGRCMRPRGKPVWGLPOLC 409
QY 410 RAGGLPRPDALFPPRLRLILFKGARYYVLARGLQVEEYPRSLQDWGIGIPEEYSGA 469
DB 410 RAGGLPRPDALFPPRLRLILFKGARYYVLARGLQVEEYPRSLQDWGIGIPEEYSGA 469
QY 470 LPRPDGSIIFPRDPRYRLDQAKLQATSGRWATELPMWGMHANSALP 520
DB 470 LPRPDGSIIFPRDPRYRLDQAKLQATSGRWATELPMWGMHANSALP 520

RESULT 14

ADAV6094 standard; protein, 520 AA.

ADAV6094;

20-NOV-2003 (first entry)

Human PRO polypeptide #72.

Human, PRO; secreted polypeptide; transmembrane polypeptide;

KW tumour necrosis factor-alpha; TNF-alpha, chondrocyte cell; tumour;
KW cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
KW liver; microvascular endothelial cell; glucose; FFA;
KW skeletal muscle cell; adipocyte cell; pericyte cell;
KW inner ear utricular supporting cell; T-lymphocyte cell;
KW endothelial cell tube formation; bone disorder; cartilage disorder;
KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; hemoglobin-associated disorder thalassemia;
KW immune system cell infiltration.
OS Homo sapiens.
PN US2003073212-A1.
XX 17-APR-2003.
PD 16-APR-2002; 2002US-00123903.
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028213.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 22-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.

20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007533.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015266.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001WO-US002706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 18-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 01-JUN-2001; 2001US-00872035.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX
 PA (GENTH) GEMENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff B, Gao W,
 PI Gerlitsen ME, Goddard A, Godowski PU, Gurney AU, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR MPI, 2003-687639/65.
 DR N-PsDB; ADA76093.
 XX
 PT New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide, designated e.g. PRO114 or PRO4978, useful in chromosome and
 PT gene mapping, in generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Claim 12; Fig 144; 659pp; English.

XX The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are

CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for modulating the uptake of
 CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
 CC stimulating differentiation of adipocyte cells, for stimulating
 CC proliferation of or gene expression in pericyte cells, for stimulating
 CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
 CC cells, for inducing endothelial cell tube formation and for treating
 CC various bone and/or cartilage disorders such as sports injuries and
 CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
 CC from cartilage are useful for treating sports-related joint problems,
 CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
 CC polypeptides are also useful for treating various mammalian haemoglobin-
 CC associated disorders such as various thalassemias and conditions which
 CC may benefit from enhanced local immune system cell infiltration. This
 CC sequence represents a human PRO polypeptide of the invention. Note: The
 CC sequence data for this patent is also available in electronic format from
 CC USPTO at seqdata.uspto.gov/sequence.html.
 XX

XX Sequence 520 AA;

Query Match 87.2%; Score 2472; DB 6; Length 520;
 Best Local Similarity 88.9%; Pred. No. 4e-218;
 Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MVARVGLLRALQLLMLKHLDAOPAEKRGQELRKBAEFLKXYGLVNBQVPAPISTRPS 60
 Db 1 MVARVGLLRALQLLMLKHLDAOPAEKRGQELRKBAEFLKXYGLVNBQVPAPISTRPS 60
 QY 61 DAIRAFQWVSQLPVSGVLDRAIRLROMTRPRCGVTDITNSYVAWAERISDLFARHRTKRRK 120
 Db 61 DAIRAFQWVSQLPVSGVLDRAIRLROMTRPRCGVTDITNSYVAWAERISDLFARHRTKRRK 120
 QY 121 KRFAQGNKMYKQHLSTYLVNMPETHLSRQFCAPCPSSCGATS--GRPS--SGRPOP 175
 Db 121 KRFAQGNKMYKQHLSTYLVNMPETHLSRQFCAPCPSSCGATS--GRPS--SGRPOP 175
 QY 176 QAPLSSGSSPSS-----KGTMTGWAMPMLMQAGAPWRPPLPRREARHPDOERSLSR 229
 Db 172 EAPAT--GPADIRLTFPGSDHNDGIGNAPDGGALAHAFPRRBAHPDQDERMSLSR 229
 QY 220 RGRNLFVVLAEHIGTTLGHTSPAPRALMAPYKRLGKDALSMQDVLAVQSLYKSPLOG 289
 Db 220 RGRNLFVVLAEHIGTTLGHTSPAPRALMAPYKRLGKDALSMQDVLAVQSLYKSPLOG 289
 QY 230 SVAVOLPEKLTFTDFETWDSYSPQGRRPETQGPKYCHSSFPDAITVDROQLYIFKGSHEWE 349
 Db 230 SVAVOLPEKLTFTDFETWDSYSPQGRRPETQGPKYCHSSFPDAITVDROQLYIFKGSHEWE 349
 QY 350 VAAADGNVEPRPDLQGRWGLPNTIEAAVSLNDGDFYFEGKRCMRPFGPKRWMLPOLC 409
 Db 350 VAAADGNVEPRPDLQGRWGLPNTIEAAVSLNDGDFYFEGKRCMRPFGPKRWMLPOLC 409
 QY 410 RAGGLPRHPDAALFPPPLRRLILFKGARYVLARGLQVPEYPSPLDQWGIPEEVSQA 469
 Db 410 RAGGLPRHPDAALFPPPLRRLILFKGARYVLARGLQVPEYPSPLDQWGIPEEVSQA 469
 QY 470 LPRPDGSIIFPRDDRWRDLQAKLQATTSGRWATELPMWGMCHANSQSALF 520
 Db 470 LPRPDGSIIFPRDDRWRDLQAKLQATTSGRWATELPMWGMCHANSQSALF 520

RESULT 15

ADA18744 standard; protein; 520 AA.

ADA18744;

20-NOV-2003 (first entry)

Human PRO polypeptide #72.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;
KW colon; breast; prostate; rectum; cervix; liver; tumour; cancer;
KW glucose uptake; FFA; adipocyte cell; pericyte cell; proteoglycan;
KW cartilage; inner ear utricular supporting cell; cytokine; A-peptide;
KW factor VIIa; endothelial cell.
XX
OS Homo sapiens.
XX
FN US2003054517-A1.
XX
PD 20-MAR-2003.
XX
PF 08-MAY-2002; 2002US-00141755.
XX
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019337.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022891.
PR 20-NOV-1998; 98WO-US022892.
PR 01-DEC-1998; 98WO-US024855.
PR 05-JAN-1999; 98WO-US025108.
PR 08-MAR-1999; 99WO-US000106.
PR 10-MAR-1999; 99WO-US000528.
PR 20-APR-1999; 99WO-US005190.
PR 14-MAY-1999; 99WO-US008615.
PR 02-JUN-1999; 99WO-US010733.
PR 01-SEP-1999; 99WO-US012252.
PR 08-SEP-1999; 99WO-US020111.
PR 13-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 05-OCT-1999; 99WO-US021547.
PR 29-NOV-1999; 99WO-US023089.
PR 30-NOV-1999; 99WO-US028214.
PR 01-DEC-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 22-DEC-1999; 99WO-US030989.
PR 30-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 03-JAN-2000; 2000WO-US000129.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 18-FEB-2000; 2000WO-US000365.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.

PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUN-2000; 2000WO-US017010.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US047259.
PR 20-DEC-2000; 2000WO-US049556.
PR 28-FEB-2001; 2001US-00828366.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001US-00892106.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX
XX (BETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z,
XX WPI, 2003-521854/49.
DR N-PDB; ADA18743.
XX
XX New PRO nucleic acid, useful for preparing a composition for treating
PT e.g., tumors.
PT
XX
PS Claim 12, Fig 144; 660p; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC prostate, rectal, cervical and liver tumours). The polynucleotides are
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA and in
CC gene therapy. The polynucleotides may also be used in preparing PRO
CC transgenic animals or knock-out animals which are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptides or antibodies are used in preparing a medicament for
CC treating a condition responsive to the polypeptides or antibodies, such

as tumours, for modulating the uptake of glucose or FFA by adipocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the release of proteoglycans from cartilage, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the release of cytokines from PBMC cells, for inhibiting the binding of A-peptide to factor VIIa, for inhibiting the differentiation of adipocyte cells and for stimulating the proliferation of endothelial cells. This sequence represents a human pro polypeptide of the invention. Note: The sequence data for this patent is also available in electronic format from USPRO at seqdata.uspto.gov/sequence.html.

CC
XX
SQ
Sequence 520 AA;

Query Match 87.2%; Score 2472; DB 6; Length 520;
Beat Local Similarity 88.9%; Pred. No. 4e-218;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MVARVGLLRALQLLLMGLDAQPAERGGQLRKEAEAFLEKGYLNEQVPKAPTSTRPS 60
DB 1 MVARVGLLRALQLLLMGLDAQPAERGGQLRKEAEAFLEKGYLNEQVPKAPTSTRPS 60
QY 61 DAIRAFQWYSQLPVSGVLDRAFLRQWTRRCGYTDTNSYAANAERISDLFARHRTKMRK 120
DB 61 DAIRAFQWYSQLPVSGVLDRAFLRQWTRRCGYTDTNSYAANAERISDLFARHRTKMRK 120
QY 121 KRFARQGNKWKYKQHLSYRLVNWPEHLRSRQFGAPCAPSSCGATS--QRWS--SGRPQ 175
DB 121 KRFARQGNKWKYKQHLSYRLVNWPEHLRSRQFGAPCAPSSCGATS--QRWS--SGRPQ 175
QY 176 QAPLTSGSPSS-----KGTITMGWAMPPLMAQAPWRTPELPKRGAEHPDODERWSLSRR 229
DB 172 EAPAT--GPADIRLTFPGQDNDGIGNAFDGPGLAHAFLPFRGEAHFDODERWSLSRR 229
QY 230 RGRNLFVYLAHEIGTGLTTHSPAPRALMAPYTKLGRDALISMDVLAVOSLYGKPLCG 289
DB 230 RGRNLFVYLAHEIGTGLTTHSPAPRALMAPYTKLGRDALISMDVLAVOSLYGKPLCG 289
QY 290 SYAVOLPGKLTDFETWDSYSPQGRRPETQGPYCHSSFDATTVDRQOOLYTFKGSHPWE 349
DB 290 SYAVOLPGKLTDFETWDSYSPQGRRPETQGPYCHSSFDATTVDRQOOLYTFKGSHPWE 349
QY 350 VAADGNVSEPRPLQERWVGLPNIIEAASVSLNDGDFYFFKGRGRCWRFRGPKPVWGLPOLC 409
DB 350 VAADGNVSEPRPLQERWVGLPNIIEAASVSLNDGDFYFFKGRGRCWRFRGPKPVWGLPOLC 409
QY 410 RAGGLPRHPDALFPPPLRRLILFKGARYYVLARGLQVEPYPRSLQDMGIPPEVSGA 469
DB 410 RAGGLPRHPDALFPPPLRRLILFKGARYYVLARGLQVEPYPRSLQDMGIPPEVSGA 469
QY 470 LPRPGSITFFPRDDRWRRLDOAKLQATTSGRWATELPMWGCHWANSGLALP 520
DB 470 LPRPGSITFFPRDDRWRRLDOAKLQATTSGRWATELPMWGCHWANSGLALP 520

Search completed: June 13, 2005, 17:58:41
Job time : 165 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 13, 2005, 17:16:46 / Search time 178 Seconds
(without alignments)
1495.962 Million cell updates/sec

Title: US-10-791-980-6
Perfect score: 2834
Sequence: 1 MVARVGLLRALQLLMGHL.....WATBLPMWGMWANSGLALF 520

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_prot:*
2: uniprot_crembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2472	87.2	520	1 MM28_HUMAN	Q9H239 homo sapien
2	2073	73.1	520	2 O8CGV8	O8CGV8 mus musculi
3	2025	71.5	510	2 O8CGV5	O8CGV5 mus musculi
4	1954	68.9	496	2 O8BG29	O8BG29 mus musculi
5	1731	61.1	393	2 O9B0G8	O9B0G8 homo sapien
6	1167	41.2	497	2 O9B0G8	O9B0G8 homo sapien
7	654	23.1	130	2 O9B0G8	O9B0G8 homo sapien
8	588	20.7	574	2 O7T2J2	O7T2J2 brachydanto
9	570	20.1	624	2 O7T2J2	O7T2J2 brachydanto
10	559	19.7	567	2 O9GTK3	O9GTK3 drosophila
11	559	19.7	570	2 O9MTL6	O9MTL6 drosophila
12	559	19.7	584	2 O9MTL6	O9MTL6 drosophila
13	559	19.7	613	2 O9W122	O9W122 drosophila
14	551.5	19.5	621	2 O7T2J1	O7T2J1 brachydanto
15	548	19.3	658	2 O7G1U8	O7G1U8 homo sapien
16	546	19.3	508	1 MM19_HUMAN	O99542 homo sapien
17	541.5	19.1	546	2 O9BTF2	O9BTF2 oryzias lat
18	540	19.1	625	2 O8B6V6	O8B6V6 homo sapien
19	540	19.1	645	1 MM24_HUMAN	O9Y512 homo sapien
20	536	18.9	618	1 MM24_HUMAN	O9Y512 homo sapien
21	535.5	18.9	607	2 O6PE06	O6PE06 rattus norv
22	534.5	18.9	607	1 MM15_HUMAN	P51512 homo sapien
23	534	18.8	669	1 MM15_HUMAN	P51512 homo sapien
24	532.5	18.8	607	1 MM16_MOUSE	O9W100 mus musculi
25	532	18.8	618	1 MM24_MOUSE	O9Y512 homo sapien
26	531.5	18.8	607	1 MM16_RAT	O9Y512 rattus norv
27	529	18.7	582	2 O9BPG1	O9BPG1 cricetus
28	527.5	18.6	576	2 O6D6C8	O6D6C8 xenopus lae
29	521.5	18.4	527	1 MM19_MOUSE	O9Y510 mus musculi
30	517.5	18.3	582	1 MM14_RAT	O10739 rattus norv
31	517.5	18.3	582	2 O8BTK2	O8BTK2 mus musculi

32	517.5	18.3	592	2 O6W5M7	O6W5M7 xenopus lae
33	517	18.2	657	1 MM15_MOUSE	O54732 mus musculi
34	516.5	18.2	582	2 O9XSP0	O9XSP0 capra hircu
35	515.5	18.2	582	2 O6DFU5	O6DFU5 mus musculi
36	514.5	18.2	582	1 MM14_HUMAN	P50281 homo sapien
37	514.5	18.2	582	1 MM14_MOUSE	P50281 mus musculi
38	512.5	18.1	582	1 MM14_RABIT	O95720 oryctolagus
39	510.5	18.0	582	2 O9GLE4	O9GLE4 bos taurus
40	509.5	18.0	580	1 MM14_PIG	O9X590 sus scrofa
41	509	18.0	613	2 O919J7	O919J7 acylchlorinu
42	501	17.7	431	2 O9BTF3	O9BTF3 oryzias lat
43	497	17.5	607	2 O7G1U7	O7G1U7 oryzias lat
44	496	17.5	608	2 O9B947	O9B947 gallus gall
45	485	17.1	562	1 MM25_HUMAN	O9npa2 homo sapien

ALIGNMENTS

RESULT 1
MM28_HUMAN STANDARD; PRT; 520 AA.
ID O9H239; O9BTF2; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Matrix metalloproteinase-28 precursor (EC 3.4.24.-) (MMP-28)
DE (Epilysin) (UniProtKB/TrEMBL)
GN Name=MMP28; Synonyms=MMP25;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=21153427; PubMed=11255011; DOI=10.1016/S0378-1119(01)00360-2;
RT Marchenko G.N., Strongin A.Y.;
RT "MMP-28, a new human matrix metalloproteinase with an unusual
RT cysteine-switch sequence is widely expressed in tumors."
RL Gene 265:87-93(2001).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Testis;
RX MEDLINE=21167821; PubMed=11213398; DOI=10.1074/jbc.M001599200;
RT Lohi J., Wilson C.L., Roby J.D., Parks W.C.;
RT "Epilysin, a novel human matrix metalloproteinase (MMP-28) expressed
RT in testis and keratinocytes and in response to injury."
RL J. Biol. Chem. 276:10134-10144(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC Southern C., Hughes S.A.;
RT "Cloning and genomic localization of a novel matrix metalloproteinase."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975109; DOI=10.1101/gr.1293003;
RT Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Bruen J.,
RT Chen J., Chow B., Chui C., Crowley C., Curran B., Deuel B., Dowd P.,
RT Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heidens S.,
RT Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RT Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RT Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagstad A.,
RT Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yamasaki D.,
RT Yi S., Yu G., Yuan J., Zhang W., Zhang Z., Goddard A., Wood W.I.,
RT Goddard P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
CC -I- FUNCTION: Can degrade casein. Could play a role in tissues
CC homeostasis and repair.
CC -I- COFACTOR: Binds 1 zinc ion per subunit, calcium (By similarity).

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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=At least 2 isoforms may be produced;
CC Name=1;
CC -1- TISSUE SPECIFICITY: Sequence=displayed;
CC low levels are detected in kidney, pancreas and lung.
CC expressed selectively in keratinocytes. Widely expressed in
CC several carcinomas as well. Is up-regulated in response to injury
CC in the skin.
CC -1- PTM: The precursor is cleaved by a furin endopeptidase (By
CC similarity).
CC -1- SIMILARITY: Belongs to the peptidase M10A family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF315683; AAC41981.1; -
DR EMBL: AF219624; AAK01480.1; -
DR EMBL: AF310002; AAK01706.1; -
DR EMBL: AY358987; AAO89346.1; -
DR HSSP: P03956; 1CGL.
DR MEROPS: M10.030; -.
DR Gene: HGNC:14366; MMP28.
DR GO: GO:0005578; C:extracellular matrix; NAS.
DR GO: GO:0004222; C:metalloendopeptidase activity; TAS.
DR GO: GO:0005508; P:proteolysis and peptidolysis; NAS.
DR InterPro: IPR000585; Hemoxen.
DR InterPro: IPR001818; Pept_M10A_M12B.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR InterPro: IPR006026; Peptidase_M.
DR InterPro: IPR009070; PGBD-like.
DR Pfam: PF00045; Hemoxen.4.
DR Pfam: PF00413; Peptidase_M10; 1.
DR Pfam: PF03933; Peptidase_M10_N; 1.
DR PRINTS: PR00138; MATRIXIN.
DR SMART: SM00120; HX; 4.
DR SMART: SM00235; ZmMc; 1.
DR PROSITE: PS00546; CYSTEINE_SWITCH; FALSE_NEG.
DR PROSITE: PS00024; HEMOXENIN; FALSE_NEG.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
KW Alternative splicing; Calcium; Extracellular matrix; Glycoprotein;
KW Hydrolase; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 22
FT PROPEP 23 122
FT CHAIN 123 520
FT DOMAIN 328 520
FT SITE 91 91
FT METAL 240 240
FT ACT SITE 241 241
FT METAL 244 244
FT METAL 250 250
FT DISULFD 324 510
FT CARBOHYD 164 164
FT CARBOHYD 355 355
FT CONFLICT 487 487
SQ SEQUENCE 520 AA; 58939 MW; E85D7ADA3069063 CRC64;
Query Match 87.2%; Score 2472; DB 1; Length 520;
Best Local Similarity 88.9%; Pred. No. 2,2e-177;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;
QY 1 MVAAGVLLRLQLLIMWHDADQPERGGQELRKEAEAFLEKRYLYNEQVPAKPTSTRFS 60
DB 1 MVAAGVLLRLQLLIMWHDADQPERGGQELRKEAEAFLEKRYLYNEQVPAKPTSTRFS 60

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QY 61 DAIRAFQWVSQLPVSGVLDRAITLRQMPFRPGVDTTNSYANMAERISDLPARHRTKMRK 120
DB 61 DAIRAFQWVSQLPVSGVLDRAITLRQMPFRPGVDTTNSYANMAERISDLPARHRTKMRK 120
QY 121 KRFAQGNKMYKQHLSTYLVNMPBEHLSRQFACAPSSCGATS---GRMS--SGRPQP 175
DB 121 KRFAQGNKMYKQHLSTYLVNMPBEHLSRQFACAPSSCGATS---GRMS--SGRPQP 175
QY 121 KRFAQGNKMYKQHLSTYLVNMPBEHLSRQFACAPSSCGATS---GRMS--SGRPQP 175
DB 121 KRFAQGNKMYKQHLSTYLVNMPBEHLSRQFACAPSSCGATS---GRMS--SGRPQP 175
QY 176 CAPLTSSGSS-----KGTITMGWNPDLMAQCAPWRTPLPRGEAHFDDEWSSLSRR 229
DB 176 CAPLTSSGSS-----KGTITMGWNPDLMAQCAPWRTPLPRGEAHFDDEWSSLSRR 229
QY 230 RGRNLFVYLAHEIGTGLTSPAPRALMAYRYKRLGDLSDMDPLAVALSTLQKPLCG 289
DB 230 RGRNLFVYLAHEIGTGLTSPAPRALMAYRYKRLGDLSDMDPLAVALSTLQKPLCG 289
QY 230 RGRNLFVYLAHEIGTGLTSPAPRALMAYRYKRLGDLSDMDPLAVALSTLQKPLCG 289
DB 230 RGRNLFVYLAHEIGTGLTSPAPRALMAYRYKRLGDLSDMDPLAVALSTLQKPLCG 289
QY 290 SVAVOLPEKLTDETDWYSYPOGRREPOTQPKYCHSSPDATVDRQOQLYIFGSHFWE 349
DB 290 SVAVOLPEKLTDETDWYSYPOGRREPOTQPKYCHSSPDATVDRQOQLYIFGSHFWE 349
QY 350 VAADGNVSEPRPLDERWVGLPRNTEAANSLNDGDFPFKRGCRWRPRGPVWGLPOLC 409
DB 350 VAADGNVSEPRPLDERWVGLPRNTEAANSLNDGDFPFKRGCRWRPRGPVWGLPOLC 409
QY 410 RAGGLPRHPDAALEFPPLRLILFKGARYVYLARGGLQVPPYPRSLQDMGGLPEEYSGA 469
DB 410 RAGGLPRHPDAALEFPPLRLILFKGARYVYLARGGLQVPPYPRSLQDMGGLPEEYSGA 469
QY 470 LPRDGSIIIPFRDRYRLDQAKLQATTSGRWATELPMWCMHANSGLALF 520
DB 470 LPRDGSIIIPFRDRYRLDQAKLQATTSGRWATELPMWCMHANSGLALF 520
RESULT 2
ID Q8GCV8 PRELIMINARY; PRT; 520 AA.
AC Q8GCV8;
DT 01-MAR-2003 (TREMREL. 23, Created)
DT 01-MAR-2003 (TREMREL. 23, Last sequence update)
DT 01-MAR-2004 (TREMREL. 26, Last annotation update)
DE Matrix metalloproteinase-28 precursor.
GN Name=Mmp28;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Heart;
RA Ilman S.A., Keski-Oja J., Lohi J.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY065653; AAL47576.1; -.
DR HSSP: P03956; 1CGL.
DR MEROPS: M10.030; -.
DR MED: MGI:2153062; Mmp28.
DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO: GO:0004222; C:metalloendopeptidase activity; IEA.
DR GO: GO:0005508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000585; Hemoxen.
DR InterPro: IPR006026; Peptidase_M.
DR InterPro: IPR001818; Pept_M10A_M12B.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR Pfam: PF00045; Hemoxen.4.
DR Pfam: PF03933; Peptidase_M10_N; 1.
DR PRINTS: PR00138; MATRIXIN.
DR SMART: SM00120; HX; 4.
DR SMART: SM00235; ZmMc; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT SIGNAL 1 22
FT CHAIN 123 520
matrix metalloproteinase-28.

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SQ SEQUENCE 520 AA; 58664 MW; 69924501CFC1991D CRC64;

Query Match 73.1%; Score 2073; DB 2; Length 520;
 Best Local Similarity 74.4%; Pred. No. 2, 2e-147;
 Matches 395; Conservative 33; Mismatches 81; Indels 22; Gaps 5;

QY 1 MVARVLLRLALQLLWGLHDAQPAERGQGLRKEAEALFKYGLNEQVPAKPTSTRS 60
 1 MVARVLLRLALQLLWGLHDAQPAERGQGLRKEAEALFKYGLNEQVPAKPTSTRS 60
 DB 1 MVARVLLRLALQLLWGLHDAQPAERGQGLRKEAEALFKYGLNEQVPAKPTSTRS 60
 61 DAIRAFQWVSQPLVSGVLDRAATLRQWTRPRCGVTDNSYAAMERISDLPARHRTQMRK 120
 DB 61 NAIRFQWVSQPLVSGVLDRAATLRQWTRPRCGVTDNSYAAMERISDLPARHRTQMRK 120
 121 KPPAKQGNKMYKQHLSTRLVWMPENLRSGFAPCAPSPSSCGATS---QRWS---SGRPOP 175
 DB 121 KPPAKQGNKMYKQHLSTRLVWMPENLRSGFAPCAPSPSSCGATS---QRWS---SGRPOP 175
 176 QAPLTSGSFSS-----KGTTWGMAMPMLAOGAPWRTPELPFRGEAHFDODERWLSRR 229
 QY 176 QAPLTSGSFSS-----KGTTWGMAMPMLAOGAPWRTPELPFRGEAHFDODERWLSRR 229
 DB 172 EAPAT--GRADIRLTFQGDHNDGLANAFDGGALAAHFLPRGEAHFDGDERWLSRR 229
 230 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALLSWDVLAVQSLYKGPLG 289
 QY 230 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALLSWDVLAVQSLYKGPLG 289
 DB 230 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALLSWDVLAVQSLYKGPLG 289
 290 SVAVALPGKLPFDFTWDSYSPQGRRPETQGRPKYCHSFDATVDRQOOLYIFKSGHFW 349
 QY 290 SVAVALPGKLPFDFTWDSYSPQGRRPETQGRPKYCHSFDATVDRQOOLYIFKSGHFW 349
 DB 290 SVAVALPGKLPFDFTWDSYSPQGRRPETQGRPKYCHSFDATVDRQOOLYIFKSGHFW 349
 350 VAADGNVSEPRPLQGRWVGLPRNIEAANVSLNDGDFYFFKGRGCMFRGPKPWGDLPOLC 409
 QY 350 VAADGNVSEPRPLQGRWVGLPRNIEAANVSLNDGDFYFFKGRGCMFRGPKPWGDLPOLC 409
 DB 350 VYVDGNVSEPRPLQGRWVGLPRNIEAANVSLNDGDFYFFKGRGCMFRGPKPWGDLPOLC 409
 410 RAGGLPRHPDALFPFPLRLRLIFKGRYYVLARGLQVEPPYPRSLQDMGGLPEEVSQA 469
 QY 410 RAGGLPRHPDALFPFPLRLRLIFKGRYYVLARGLQVEPPYPRSLQDMGGLPEEVSQA 469
 DB 410 RAGGLPRHPDALFPFPLRLRLIFKGRYYVLARGLQVEPPYPRSLQDMGGLPEEVSQA 469
 470 LRPDGSIIFFRDDRWRDLQAKLTATSGRWATELPMWGCWHSNAGSALF 520
 QY 470 LRPDGSIIFFRDDRWRDLQAKLTATSGRWATELPMWGCWHSNAGSALF 520
 DB 470 LRPDGSIIFFRDDRWRDLQAKLTATSGRWATELPMWGCWHSNAGSALF 520

RESULT 3
 O8BGV5 PRELIMINARY; PRT; 510 AA.

AC O8BGV5;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Matrix metalloproteinase-28 variant A precursor.
 GN Name=Mmp28;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Heart;
 RA Ilman S.A., Keski-Oja J., Lohi J.;
 DT Submitted (DEC-2001) to the EMBL/GenBank/DBJ database.
 DR EMBL; AY071828; AAL57761.1; -
 DR HSSP; P03956; 1CGL.
 DR MEROPS; M10.010; -
 DR MGD; MGI:2253062; Mmp28.
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR006058; Hemoxen.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR009070; PGBD_like.

DR Pfam; PF00045; Hemoxen; 4.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00138; MATRILIN.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZMOC; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN 123 510 Potential.
 FT matrix metalloproteinase-28 variant A precursor.

SQ SEQUENCE 510 AA; 57371 MW; 3479A65940835E93 CRC64;

Query Match 71.5%; Score 2025; DB 2; Length 510;
 Best Local Similarity 73.3%; Pred. No. 8, 6e-144;
 Matches 389; Conservative 31; Mismatches 79; Indels 32; Gaps 6;

QY 1 MVARVLLRLALQLLWGLHDAQPAERGQGLRKEAEALFKYGLNEQVPAKPTSTRS 60
 1 MVARVLLRLALQLLWGLHDAQPAERGQGLRKEAEALFKYGLNEQVPAKPTSTRS 60
 DB 1 MVARVLLRLALQLLWGLHDAQPAERGQGLRKEAEALFKYGLNEQVPAKPTSTRS 60
 61 DAIRAFQWVSQPLVSGVLDRAATLRQWTRPRCGVTDNSYAAMERISDLPARHRTQMRK 120
 QY 61 NAIRFQWVSQPLVSGVLDRAATLRQWTRPRCGVTDNSYAAMERISDLPARHRTQMRK 120
 DB 61 NAIRFQWVSQPLVSGVLDRAATLRQWTRPRCGVTDNSYAAMERISDLPARHRTQMRK 120
 121 KPPAKQGNKMYKQHLSTRLVWMPENLRSGFAPCAPSPSSCGATS---QRWS---SGRPOP 175
 QY 121 KPPAKQGNKMYKQHLSTRLVWMPENLRSGFAPCAPSPSSCGATS---QRWS---SGRPOP 175
 DB 121 KPPAKQGNKMYKQHLSTRLVWMPENLRSGFAPCAPSPSSCGATS---QRWS---SGRPOP 175
 176 QAPLTSGSFSS-----KGTTWGMAMPMLAOGAPWRTPELPFRGEAHFDODERWLSRR 229
 QY 176 QAPLTSGSFSS-----KGTTWGMAMPMLAOGAPWRTPELPFRGEAHFDODERWLSRR 229
 DB 172 EAPAT--GRADIRLTFQGDHNDGLANAFDGGALAAHFLPRGEAHFDGDERWLSRR 229
 230 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALLSWDVLAVQSLYKGPLG 289
 QY 230 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALLSWDVLAVQSLYKGPLG 289
 DB 230 RGRNLFVYLAHEIGHTLGLTHSPAPRALMAPYKRLGRDALLSWDVLAVQSLYKGPLG 289
 290 SVAVALPGKLPFDFTWDSYSPQGRRPETQGRPKYCHSFDATVDRQOOLYIFKSGHFW 349
 QY 290 SVAVALPGKLPFDFTWDSYSPQGRRPETQGRPKYCHSFDATVDRQOOLYIFKSGHFW 349
 DB 290 SVAVALPGKLPFDFTWDSYSPQGRRPETQGRPKYCHSFDATVDRQOOLYIFKSGHFW 349
 350 VAADGNVSEPRPLQGRWVGLPRNIEAANVSLNDGDFYFFKGRGCMFRGPKPWGDLPOLC 409
 QY 350 VAADGNVSEPRPLQGRWVGLPRNIEAANVSLNDGDFYFFKGRGCMFRGPKPWGDLPOLC 409
 DB 350 VYVDGNVSEPRPLQGRWVGLPRNIEAANVSLNDGDFYFFKGRGCMFRGPKPWGDLPOLC 409
 410 RAGGLPRHPDALFPFPLRLRLIFKGRYYVLARGLQVEPPYPRSLQDMGGLPEEVSQA 469
 QY 410 RAGGLPRHPDALFPFPLRLRLIFKGRYYVLARGLQVEPPYPRSLQDMGGLPEEVSQA 469
 DB 410 RAGGLPRHPDALFPFPLRLRLIFKGRYYVLARGLQVEPPYPRSLQDMGGLPEEVSQA 469
 470 LRPDGSIIFFRDDRWRDLQAKLTATSGRWATELPMWGCWHSNAGSALF 520
 QY 470 LRPDGSIIFFRDDRWRDLQAKLTATSGRWATELPMWGCWHSNAGSALF 520
 DB 460 LRPDGSIIFFRDDRWRDLQAKLTATSGRWATELPMWGCWHSNAGSALF 510

RESULT 4
 O8BG29 PRELIMINARY; PRT; 496 AA.

AC O8BG29;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Matrix metalloproteinase-28 variant B precursor (Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:DJ10023p12 product:matrix metalloproteinase 28 (epilysin), full insert sequence).
 GN Name=Mmp28;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Heart;
 RA Ilman S.A., Keski-Oja J., Lohi J.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 403:685-690(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RA The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 Kono H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashigagi K.,
 Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RA Aichi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 Hori F., Imctani K., Ishii Y., Itoh M., Kagawa I., Kaubuka T.,
 Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 Tagawa A., Takahashi F., Takaku-Akehira S., Takeda Y., Tanaka T.,
 Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AV071829; AAL57762.1; -;
 DR EMBL: AK051258; BAC34577.1; -;
 DR HSP: P03956; ICGL.
 DR MEROPS: M10.030; -;
 DR MGD: MGI:2153062; Mmp28.
 DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO: GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO: GO:0005508; F:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR000585; Hemopexin.
 DR InterPro: IPR006026; Peptidase M.
 DR InterPro: IPR001818; Pept_M10A_M12B.
 DR InterPro: IPR006025; Pept_M_zn_BS.

DR InterPro: IPR009070; PGSD 11ke.
 DR Pfam: PF00045; Hemopexin_3.
 DR Pfam: PF03933; Peptidase_M10_N; 1.
 DR PRINTS: PR00138; MATRIXIN.
 DR SMART: SM00120; HX; 3.
 DR SMART: SM00235; Zmc; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KM SIGNAL.
 FT SIGNAL.
 FT CHAIN 123 496 potential.
 FT matrix metalloproteinase-28 variant B
 FT precursor.
 SQ SEQUENCE 496 AA; 55829 MW; CEE16CD0F0D2906D CRC64;
 Query Match 68.9%; Score 1954; DB 2; Length 496;
 Best local similarity 71.2%; Pred. No. 1.8e-138;
 Matches 378; Conservative 30; Mismatches 77; Indels 46; Gaps 6;
 QY 1 MYARVGLLRALQLLWGHLDPAERGGQELRKAENAFLEKYGYNQVAPKPTSTFS 60
 DB 1 MYAGVSLLRALPLILWGCDAQPTQHGRLPRLQEAFLFKYGLYSQSKAPASQFR 60
 QY 61 DAIRAFQVSQLPVSGVLDRAITLQMTPRRCGVDTNYSYAMARISDLFAHRTKRRK 120
 DB 61 NAIRFQVSQLPVSGVLDRAITLQMTPRRCGVADTSHATWTERISTLLAGHRAKRRK 120
 QY 121 KRFAQGNKMYKQHLSTYLVMPPEHLRSRQFACAPSSCGATS---QRMS--SGRPOP 175
 DB 121 KRFAKPGKMYKQHLSTYLVMPPEHLRSRQFACAPSSCGATS---QRMS--SGRPOP 175
 QY 176 QAPLTSGSPSS-----KGTTWGMAMPVLAQGAQWPTPLPRRGAHFQDERWSLSRR 229
 DB 172 EAPAT--GPADIRLTFQGHNDGIANAFDQGGALAAFLPRRGAHFQDERWSLSRR 229
 QY 230 RGRNLFVYLAHEIGHTGLTSPAPRALMAPYKRGDRLLGMDVLAQVSYXKRLG 289
 DB 230 RGRNLFVYLAHEIGHTGLTSPAPRALMAPYKRGDRLLGMDVLAQVSYXKRLG 289
 QY 290 SVAQVLPGLFTDEFTWDSYSPQGRREPQPKYCHSSPDATVDRQQQLYIKGSHFWE 349
 DB 290 SVAQVLPGLFTDEFTWDSYSPQGRREPQPKYCHSSPDATVDRQQQLYIKGSHFWE 349
 QY 350 VAADGVNSEPRPLQERVGVLPVNIETAAVSLNCDPTFFRGKCMWRPGRKPVGLPOLC 409
 DB 354 -----EPRPLQKMRPGLPPIEAAVSLNCDPTFFRGKCMWRPGRKPVGLPOLC 409
 QY 410 RAGGLPRHPDALFFPPLRLILFKGARVYVLAARGLOVPEYPRSLQDQGIPEEYSGA 469
 DB 386 RAGGLPRHPDALFFPPLRLILFKGARVYVLAARGLOVPEYPRSLQDQGIPEEYSGA 469
 QY 470 LRPDGSITFRDRIWRDLQATLQATTSGRWATELPMWGMHANSGLALF 520
 DB 446 LRPDGSITFRDRIWRDLQATLQATTSGRWATELPMWGMHANSGLALF 520
 DB 446 LRPDGSITFRDRIWRDLQATLQATTSGRWATELPMWGMHANSGLALF 520
 RESULT 5
 ID 09BUC8 PRELIMINARY; PRT; 393 AA.
 AC 09BUC8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Matrix metalloproteinase 28, preproprotein isoform 2.
 GN Name:MMP28;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RN Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002631; AA02631.1; -.
DR HSSP; P03956; 1CGI.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopekin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; RGD-like.
DR Pfam; PF000645; Hemopekin_1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SO SEQUENCE 393 AA; 4469 MW; 07D443B5401699 CRC64;

Query Match 61.1%; Score 1731; DB 2; Length 393;
Best Local Similarity 85.2%; Pred. No. 7.9e-122;
Matches 341; Conservative 4; Mismatches 33; Indels 22; Gaps 5;
DB 1 MVARVGLLRALQLLMGHLDAPARCGOELKBAEPLKXGYLNEQVPAKPTSTRS 60
QY 1 MVARVGLLRALQLLMGHLDAPARCGOELKBAEPLKXGYLNEQVPAKPTSTRS 60
DB 1 MVARVGLLRALQLLMGHLDAPARCGOELKBAEPLKXGYLNEQVPAKPTSTRS 60
QY 61 DAIRAFQWVSQLPVSGLDRAATRRQMTTRPCGVTDNNSYAAAEISDLFARHTQMRK 120
DB 61 DAIRAFQWVSQLPVSGLDRAATRRQMTTRPCGVTDNNSYAAAEISDLFARHTQMRK 120
QY 121 KRPFAKGNKMYKOHLSYRLVNPBEHLRSQFGAPCAPSSCGATS---QWS--SGRPOP 175
DB 121 KRPFAKGNKMYKOHLSYRLVNPBEHLRSQFGAPCAPSSCGATS---QWS--SGRPOP 175
QY 121 KRPFAKGNKMYKOHLSYRLVNPBEHLRSQFGAPCAPSSCGATS---QWS--SGRPOP 175
DB 121 KRPFAKGNKMYKOHLSYRLVNPBEHLRSQFGAPCAPSSCGATS---QWS--SGRPOP 175
QY 176 QAPLTGSGSBS-----KGTTMGMAMPMLAQAQAPRTPLPRGGAHPQDNRSLSR 229
DB 176 QAPLTGSGSBS-----KGTTMGMAMPMLAQAQAPRTPLPRGGAHPQDNRSLSR 229
QY 176 QAPLTGSGSBS-----KGTTMGMAMPMLAQAQAPRTPLPRGGAHPQDNRSLSR 229
DB 176 QAPLTGSGSBS-----KGTTMGMAMPMLAQAQAPRTPLPRGGAHPQDNRSLSR 229
QY 230 RGRNLFVYLAHEIGTTLGTLSPAPRALMAPYKRLGRDALLSMQDVLAVQSYKPLG 289
DB 230 RGRNLFVYLAHEIGTTLGTLSPAPRALMAPYKRLGRDALLSMQDVLAVQSYKPLG 289
QY 230 RGRNLFVYLAHEIGTTLGTLSPAPRALMAPYKRLGRDALLSMQDVLAVQSYKPLG 289
DB 230 RGRNLFVYLAHEIGTTLGTLSPAPRALMAPYKRLGRDALLSMQDVLAVQSYKPLG 289
QY 290 SVAVALPGKLTFTDFTWDSYSPQGRRPETGPRYCHSSPDAITVDRQQLYIFKSHFWE 349
DB 290 SVAVALPGKLTFTDFTWDSYSPQGRRPETGPRYCHSSPDAITVDRQQLYIFKSHFWE 349
QY 290 SVAVALPGKLTFTDFTWDSYSPQGRRPETGPRYCHSSPDAITVDRQQLYIFKSHFWE 349
DB 290 SVAVALPGKLTFTDFTWDSYSPQGRRPETGPRYCHSSPDAITVDRQQLYIFKSHFWE 349
QY 350 VAADGVNSBPRPLQERWVGLPNIIEAAVSLNDGDFEFK 389
DB 350 VAADGVNSBPRPLQERWVGLPNIIEAAVSLNDGDFEFK 389

RESULT 6
ID 06P714 PRELIMINARY; PRT; 497 AA.
AC 06P714;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE MGC68506 protein.
OS Name=MGC68506;
GN Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RL Klein S., Strausberg R.;
RN Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061659; AA061659.1; -.
DR HSSP; P08254; 1B3D.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopekin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; RGD-like.
DR Pfam; PF000645; Hemopekin_1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00120; HK; 4.
DR PROSITE; PS00235; ZmC; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SO SEQUENCE 497 AA; 57096 MW; 3D6BA00FB3BD2205 CRC64;

Query Match 41.2%; Score 1167; DB 2; Length 497;
Best Local Similarity 47.8%; Pred. No. 2.7e-79;

Query Match	19.7%;	Score 559;	DB 2;	Length 567;
Best Local Similarity	30.4%;	Pred. No. 1.6e-33;		
Matches 158; Conservative	74;	Mismatches 200;	Inde1s	88. Cans 18.

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QY 3EAAFEKXGYLNEOVQAPFJSTRSD-----AIRAFQWSQLPVSGVLDRLATRLQOMTR 88
Db 58QATVYSQGYLPABA-RNPASSGLHDRTVSAIEEFQSFAGINTGELDEMTIKMSL 116
QY 89PRGCVTDTSYAAMERISDLFAHRHTMRKKRFAQOGKWKYKOH,SYRLVWPEHRS 148
Db 117PRGCVAD-----RNGODSHSKRYALQGSRMVKNUTYKISKTPRLKR 160
QY 149RQCGAPCAPSPSCGATSQRMSSGRPOALPTSC-----SPSSKGTMMGMAMPL 198
Db 161VDVDA-----EIGAPAVWSEDTDLFTTRKTSPPAIEIKFVSESHGDAFPD----- 209
QY 199MAOGAPWRTPLP-RGEAHFDODERWSLSRRGRNLFWLAIEHTGLHSPARAL 257
Db 210--QGGLTAAFPFVPGDAHFDADAELWTISPGPTNLFVQANRPHSHGLSHSQSAL 267
QY 258MAPYKRLGRDALLSMQVLAVGLYKGPJGGSVANQLPEKLFTEFTWDSYSPQGRPE 317
Db 268MAPFRGEPVFKLDEDDKKAITOSLYRKTN-----QLPPTVYPAITORPYSP----- 316
QY 318TQGPK-----YC-HSFPDAITVDRQOOLYFKGSHFWEVADGNVSE--PRPLOERWVG 366
Db 317---PKVPLDSDICKDSKVDTLFNBSAQEYTAFFGDKRYKLLTD-SVEEYRQOLISKMPG 372
QY 369LEPNLEAAVSLNNGDPFFPKGRCMRFRGPKVWGLPOLCRAG--GLPRHPDAALFFPP 426
Db 373LEPNID-NAFTYKNGKTYFFKGTQYMWYQORQMDGVYPRKEISEGTGIPDHLDAAWVG 431
QY 427LRRLLEFKGARVYVILANGUL-OVEPYPRSLQOMGCIPEEVSGLPRPDGSIIFPRDRY 485
Db 432NGKIFYFGSKFMBFDPADKRPVYASYPKISIMBEBVNNDALAKTYNGTYTFFKODKY 491
QY 486WRLOAKYQAT-----SGRWAELEPMGCMHANSQS 517
Db 492YRFHDARPAVDSATPPRPPTAH-----WFGCKNTPBST 526

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RESULT 11	
Q8MLN6	
ID	PRELIMINARY;
Q8MLN6	PRT;
	570 AA

AC OGMN:NG-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE CG4859-PB.
GN Name=Mmp1; ORFNames=CG4859;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Empidoidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132, DOI=10.1126/science.287.5461.2185
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blaise J.R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Abmayant A., An H.U., Andrews-Plamkoc C., Baldwin D.,
RA Ballew R.M., Baas A., Bakendste J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.U., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.J., Gu Z., Guan P., Harris M.,
RA Harris N.D., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Jorgensen C.,
RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobery C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleby J.M.,
RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svaydas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock R.M., Weisenbach J.,
RA Williams S.M., Woodagst, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleby J.M., Pak S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svaydas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock R., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svaydas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.,
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002)

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RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=2242609; PubMed=12537572;
RA Mlera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Slach C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu U., Berman B.P.,
RA Bettencourt B.R., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003464; AAM68327.1; -.
DR HSSP; P03956; ICGL.
DR MEROPS; M10.031; -.
DR FlyBase; FBgn0035049; Mmp1.
DR GO; GO:0044222; P:metalloendopeptidase activity; TAS.
DR GO; GO:0048102; P:autophagic cell death; IEP.
DR GO; GO:0035001; P:dorsal trunk growth; IMP.
DR GO; GO:0002168; P:lateral development (sensu Insecta); IMP.
DR GO; GO:0035071; P:salivary gland cell death; IEP.
DR InterPro; IPR00585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M10A_M12B.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; Znmc; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
DR SEQUENCE 570 AA; 63484 MW; 902DCF91974CF0BD CRC64;
SQ
Query Match 19.7%; Score 559; DB 2; Length 570;
Best Local Similarity 30.4%; Pred. No. 1.6e-33;
Matches 158; Conservative 74; Mismatches 200; Indels 88; Gaps 18;

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DB 376 LPGAID-AAFTYKNGKTYFFKGTQYWRYOGRQMDGVYPKIESEGFRTIPIHLDAAWYWG 434
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DT 01-OCT-2002 (Tremblrel, 22, Created)
DT 01-OCT-2002 (Tremblrel, 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel, 26, Last annotation update)
DE R862222P.
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OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
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RG STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Abdayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Fafan D., Faise E.,
RA George R., Gonzalez M., Guarini H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Paclab J., Parasas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY118405; AAM48434.1; -.
DR HSSP; P03956; ICGL.
DR MEROPS; M10.031; -.
DR FlyBase; FBgn0035049; Mmp1.
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DR GO; GO:0048102; P:autophagic cell death; IEP.
DR GO; GO:0035001; P:dorsal trunk growth; IMP.
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DR GO; GO:0035071; P:salivary gland cell death; IEP.
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DR InterPro; IPR006025; Pept_M10A_M12B.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; Znmc; 1.
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Best Local Similarity 30.4%; Pred. No. 1.7e-33;
Matches 158; Conservative 74; Mismatches 200; Indels 88; Gaps 18;

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 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
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 GN Name=Mmp1; ORFNames=CG4859;
 OS Drosophila melanogaster (Fruit fly).
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 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
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RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,
 RA Baller R.M., Bau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Botkova D., Botchan M.R., Boulter J., Brokstein P., Brotter P.,
 RA Butts K.C., Busam D.A., Butler H., Brokstein P., Brokstein P.,
 RA Cherly J.M., Cawley S., Dahlke C., Fentz C., Fentz C., Fentz C.,
 RA de Pallos B., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fierliera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegyan C.,
 RA Jaiswal M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "the genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Swirekas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Venter C., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "finishing a whole-genome shotgun: Release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.

RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomes perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;
 RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Belencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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 RP SEQUENCE FROM N.A.

RG Flybase;
 RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
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 RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
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 DR GO; GO:0004222; F:metalloendopeptidase activity; TAS.
 DR GO; GO:0048102; P:autophagic cell death; IMP.
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 DR GO; GO:0035071; P:larval development (sensu Insecta); IMP.
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GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: June 13, 2005, 17:27:41 ; Search time 43 Seconds
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Title: US-10-791-980-6

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2472	87.2	520	US-09-950-510-21	Sequence 21, Appli
4	2472	87.2	520	US-09-950-510-24	Sequence 24, Appli
5	2444	86.2	520	US-09-391-104-10	Sequence 10, Appli
6	2324.5	82.0	445	US-09-950-510-12	Sequence 12, Appli
7	2207	77.9	469	US-09-950-510-23	Sequence 23, Appli
8	1731	61.1	393	US-09-950-510-22	Sequence 22, Appli
9	546	19.3	508	US-09-171-545-1	Sequence 1, Appli
10	543	19.2	508	US-09-391-104-18	Sequence 18, Appli
11	542	19.1	517	US-09-171-545-2	Sequence 2, Appli
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ALIGNMENTS

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Sequence 6, Application US/09862631									
Patent No. 6734005									
GENERAL INFORMATION:									
APPLICANT: Holmgren, Erik									
APPLICANT: Kihlen, Mats									
APPLICANT: Wood, Tim									
APPLICANT: Ekblom, Jonas									
TITLE OF INVENTION: No. 6734005e1 Matrix Metalloproteinases									
FILE REFERENCE: 00014iregus									
CURRENT APPLICATION NUMBER: US/09/862,631									
CURRENT FILING DATE: 2000-05-22									
PRIOR APPLICATION NUMBER: 206119									
NUMBER OF SEQ ID NOS: 8									
SOFTWARE: PatentIn version 3.0									
SEQ ID NO 6									
LENGTH: 520									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-09-862-631-6									
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Matches 520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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; Patent No. 6740514
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory
; TITLE OF INVENTION: 46798, A No. 6740514e1 Human Matrix Metalloproteinase And Uses Th
; FILE REFERENCE: 10147-45U1
; CURRENT APPLICATION NUMBER: US/09/950,510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/251,156
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-510-2

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; Sequence 21, Application US/09950510
; Patent No. 6740514
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory
; TITLE OF INVENTION: 46798, A No. 6740514e1 Human Matrix Metalloproteinase And Uses Th
; FILE REFERENCE: 10147-45U1
; CURRENT APPLICATION NUMBER: US/09/950,510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/251,156
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-510-21

Query Match 87.2%; Score 2472; DB 4; Length 520;
Best Local Similarity 88.9%; Pred. No. 8.9e-238;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

Qy 1 MVARVGLLRALQLLMLGHLDQPAERGGQELRKEAEFLKGYLNEQVPAKPTSTFS 60
Db 1 MVARVGLLRALQLLMLGHLDQPAERGGQELRKEAEFLKGYLNEQVPAKPTSTFS 60
Qy 61 DAIRAFQWSQLPVSGVLDRAATLRQMTPRCGVTDNSYAAMERISDLFAHRTKMRK 120
Db 61 DAIRAFQWSQLPVSGVLDRAATLRQMTPRCGVTDNSYAAMERISDLFAHRTKMRK 120
Qy 121 KRPAKQGNKMYKQHLSTYRLVNWPEHLRSRQFAPCAPSSCGATS--QRWS--SGRPQ 175
Db 121 KRPAKQGNKMYKQHLSTYRLVNWPEHLRSRQFAPCAPSSCGATS--QRWS--SGRPQ 175
Qy 176 QAPLTSGPS--KTTTGMAMPMAOGAEWRTPFLPRRGEAHFDODERMSLSRR 229
Db 176 QAPLTSGPS--KTTTGMAMPMAOGAEWRTPFLPRRGEAHFDODERMSLSRR 229
Qy 230 RGRNLFVYLAHEIGTGLTTHSPAPRALMAPYKRLGDALISMDVLAVOSLYGKPLG 289
Db 230 RGRNLFVYLAHEIGTGLTTHSPAPRALMAPYKRLGDALISMDVLAVOSLYGKPLG 289
Qy 290 SVAVOLPGKLTFTDFTWDSYSPQGRRPETQPKYCHSSFDATYDROQOLYIFKGSHPWE 349
Db 290 SVAVOLPGKLTFTDFTWDSYSPQGRRPETQPKYCHSSFDATYDROQOLYIFKGSHPWE 349
Qy 350 VAAQGNVSEPRPLOBRWGLPNTIEAAVSLNDGFYFKGRCWFRGPKPVWGLPOLC 409
Db 350 VAAQGNVSEPRPLOBRWGLPNTIEAAVSLNDGFYFKGRCWFRGPKPVWGLPOLC 409
Qy 410 RAGGLPRHPDALFFPPLRLILFKGARYYVLARGLQVEPYPRSLQDWGIPBEVSGA 469
Db 410 RAGGLPRHPDALFFPPLRLILFKGARYYVLARGLQVEPYPRSLQDWGIPBEVSGA 469
Qy 470 LPRPDGSIIFRDRYWRRLDQAKLQATTSGRWATELPMWGCWHAHNSGSLAF 520
Db 470 LPRPDGSIIFRDRYWRRLDQAKLQATTSGRWATELPMWGCWHAHNSGSLAF 520

RESULT 4
US-09-950-510-24
; Sequence 24, Application US/09950510
; Patent No. 6740514
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory
; TITLE OF INVENTION: 46798, A No. 6740514e1 Human Matrix Metalloproteinase And Uses Th
; FILE REFERENCE: 10147-45U1
; CURRENT APPLICATION NUMBER: US/09/950,510
; CURRENT FILING DATE: 2001-09-10
```

;; PRIOR APPLICATION NUMBER: 60/251,156
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 24
;; LENGTH: 520
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-950-510-24

Query Match 87.2%; Score 2472; DB 4; Length 520;
Best Local Similarity 88.9%; Pred. No. 8,9e-238;
Matches 472; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

QY 1 MVARVGLLRALQLLMGLHDAQPAERGGQELRKEAEFLKGYGLNEQVPKAPTSTPS 60
DB 1 MVARVGLLRALQLLMGLHDAQPAERGGQELRKEAEFLKGYGLNEQVPKAPTSTPS 60
QY 61 DAIRAFQWVSQLPVSGVLDRAITLRQMTTRPCGVTDNTSYAAMAEKISDLFAHRTKMRK 120
DB 61 DAIRAFQWVSQLPVSGVLDRAITLRQMTTRPCGVTDNTSYAAMAEKISDLFAHRTKMRK 120
QY 121 KRFPAQGNKMYKQHLSTYRLVNMPEHLRSKQFAPCAPSSCGATS--GRSPQ 175
DB 121 KRFPAQGNKMYKQHLSTYRLVNMPEHLRSKQFAPCAPSSCGATS--GRSPQ 175
QY 176 QAPLTSGSPSS-----KGTITMGWAMPMAQGAEMRTPEFLPRGEAHFDODERMSLSR 229
DB 172 EAPAT--GPADIRLTFPGQDNDGLGNAPDQGGALAAFLPRGGAHFDODERMSLSR 229
QY 230 RGRNLFVVLAEHIGTLGLTSHSPAPRALMAPYKRLGSDALISWDVLAVQSLYKGPILG 289
DB 230 RGRNLFVVLAEHIGTLGLTSHSPAPRALMAPYKRLGSDALISWDVLAVQSLYKGPILG 289
QY 290 SVAVOLPGKLFDFEFTWDSYSPQGRRPETQGPYCHSSFDATTVROOOLYIFKSHFWE 349
DB 290 SVAVOLPGKLFDFEFTWDSYSPQGRRPETQGPYCHSSFDATTVROOOLYIFKSHFWE 349
QY 350 VAADGNVSEPRPQERWVGLPPIIEAAVSLNDGDFYFFKGGRCMRFRGPKVWGILPOLC 409
DB 350 VAADGNVSEPRPQERWVGLPPIIEAAVSLNDGDFYFFKGGRCMRFRGPKVWGILPOLC 409
QY 410 RAGGLPRHPDAAFLPPLRLILFKGARYYVLARGLQVEPPYPSLQDWGIPREVSGA 469
DB 410 RAGGLPRHPDAAFLPPLRLILFKGARYYVLARGLQVEPPYPSLQDWGIPREVSGA 469
QY 470 LRPDGSIIFFRDRIYRLDQAKLQATTSGRWATELPMWGMCHANSGLALF 520
DB 470 LRPDGSIIFFRDRIYRLDQAKLQATTSGRWATELPMWGMCHANSGLALF 520

RESULT 5

US-09-391-104-10
;; Sequence 10, Application US/09391104
;; Patent No. 639371
;; GENERAL INFORMATION:
;; APPLICANT: Abbott Laboratories
;; APPLICANT: Falduto, Michael T.
;; APPLICANT: Magnuson, Scott R.
;; APPLICANT: Morgan, Douglas W.
;; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
;; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
;; TITLE OF INVENTION: OF USING SAME
;; FILE REFERENCE: 6073.US.P1
;; CURRENT APPLICATION NUMBER: US/09/391,104
;; CURRENT FILING DATE: 1999-09-07
;; PRIOR APPLICATION NUMBER: US 08/814,394
;; PRIOR FILING DATE: 1997-03-11
;; NUMBER OF SEQ ID NOS: 35
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10
;; LENGTH: 520
;; TYPE: PRT

;; ORGANISM: Homo sapiens
US-09-391-104-10

Query Match 86.2%; Score 2444; DB 3; Length 520;
Best Local Similarity 87.9%; Pred. No. 5,6e-235;
Matches 467; Conservative 7; Mismatches 35; Indels 22; Gaps 5;

QY 1 MVARVGLLRALQLLMGLHDAQPAERGGQELRKEAEFLKGYGLNEQVPKAPTSTPS 60
DB 1 MVARVGLLRALQLLMGLHDAQPAERGGQELRKEAEFLKGYGLNEQVPKAPTSTPS 60
QY 61 DAIRAFQWVSQLPVSGVLDRAITLRQMTTRPCGVTDNTSYAAMAEKISDLFAHRTKMRK 120
DB 61 DAIRAFQWVSQLPVSGVLDRAITLRQMTTRPCGVTDNTSYAAMAEKISDLFAHRTKMRK 120
QY 121 KRFPAQGNKMYKQHLSTYRLVNMPEHLRSKQFAPCAPSSCGATS--GRSPQ 175
DB 121 KRFPAQGNKMYKQHLSTYRLVNMPEHLRSKQFAPCAPSSCGATS--GRSPQ 175
QY 176 QAPLTSGSPSS-----KGTITMGWAMPMAQGAEMRTPEFLPRGEAHFDODERMSLSR 229
DB 172 EAPAT--GPADIRLTFPGQDNDGLGNAPDQGGALAAFLPRGGAHFDODERMSLSR 229
QY 230 RGRNLFVVLAEHIGTLGLTSHSPAPRALMAPYKRLGSDALISWDVLAVQSLYKGPILG 289
DB 230 RGRNLFVVLAEHIGTLGLTSHSPAPRALMAPYKRLGSDALISWDVLAVQSLYKGPILG 289
QY 290 SVAVOLPGKLFDFEFTWDSYSPQGRRPETQGPYCHSSFDATTVROOOLYIFKSHFWE 349
DB 290 SVAVOLPGKLFDFEFTWDSYSPQGRRPETQGPYCHSSFDATTVROOOLYIFKSHFWE 349
QY 350 VAADGNVSEPRPQERWVGLPPIIEAAVSLNDGDFYFFKGGRCMRFRGPKVWGILPOLC 409
DB 350 VAADGNVSEPRPQERWVGLPPIIEAAVSLNDGDFYFFKGGRCMRFRGPKVWGILPOLC 409
QY 410 RAGGLPRHPDAAFLPPLRLILFKGARYYVLARGLQVEPPYPSLQDWGIPREVSGA 469
DB 410 RAGGLPRHPDAAFLPPLRLILFKGARYYVLARGLQVEPPYPSLQDWGIPREVSGA 469
QY 470 LRPDGSIIFFRDRIYRLDQAKLQATTSGRWATELPMWGMCHANSGLALF 520
DB 470 LRPDGSIIFFRDRIYRLDQAKLQATTSGRWATELPMWGMCHANSGLALF 520

RESULT 6

US-09-950-510-12
;; Sequence 12, Application US/09950510
;; Patent No. 6740514
;; GENERAL INFORMATION:
;; APPLICANT: Curtis, Rory
;; TITLE OF INVENTION: 46798, A No. 6740514el Human Matrix Metalloproteinase And Uses Th
;; FILE REFERENCE: 10147-45U1
;; CURRENT APPLICATION NUMBER: US/09/950,510
;; CURRENT FILING DATE: 2001-09-10
;; PRIOR APPLICATION NUMBER: 60/251,156
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 12
;; LENGTH: 445
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-950-510-12

Query Match 82.0%; Score 2324,5; DB 4; Length 445;
Best Local Similarity 84.8%; Pred. No. 3,7e-223;
Matches 441; Conservative 1; Mismatches 3; Indels 75; Gaps 2;

QY 1 MVARVGLLRALQLLMGLHDAQPAERGGQELRKEAEFLKGYGLNEQVPKAPTSTPS 60
DB 1 MVARVGLLRALQLLMGLHDAQPAERGGQELRKEAEFLKGYGLNEQVPKAPTSTPS 60
QY 61 DAIRAFQWVSQLPVSGVLDRAITLRQMTTRPCGVTDNTSYAAMAEKISDLFAHRTKMRK 120

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Db      61 DAIRAFQWVSQLPVSGVLDRAITLROMTRPCGVTDITNSYAAMERISDLFARRHTKMRK 120
Qy      121 KRPAKQGNKWKYKQHLSTYLVNMPHEHLNRQFGACAPSSCGANSQMSGRGPQAPLPT 180
Db      121 KRPAKQG-----GALAH-----132
Qy      181 SGSSSKGTTTGMAMPIMAGAPWRTPFLPRGSAHFDDERWLSRRGRNLFVTLAH 240
Db      133 -----AFLEPRGEAHPDODERWLSRRGRNLFVTLAH 165
Qy      241 EIGHTLGLTHSPAPRALMAPYKRLGRDALISWDVLAQVSLKVPFGSSVANVLPGKLF 300
Db      166 EIGHTLGLTHSPAPRALMAPYKRLGRDALISWDVLAQVSLKVPFGSSVANVLPGKLF 225
Qy      301 TDFETWDSYSPQGRRPETQGPKYCHSSFDAITVDROOQLYIFKGSHEWEVAADGANSEPP 360
Db      226 TDFETWDSYSPQGRRPETQGPKYCHSSFDAITVDROOQLYIFKGSHEWEVAADGANSEPP 285
Qy      361 PLOERWVGLPPTNFAAVALNDGDFYFKGRCMRFRGPKPVGWGLPOLCRAGGLPRHPDA 420
Db      286 PLOERWVGLPPTNFAAVALNDGDFYFKGRCMRFRGPKPVGWGLPOLCRAGGLPRHPDA 345
Qy      421 ALFEPPLRLILFKGARYYVLARGGLQVEPYPRSLQDWGIDEVYSGALPREDSITFF 480
Db      346 ALFEPPLRLILFKGARYYVLARGGLQVEPYPRSLQDWGIDEVYSGALPREDSITFF 405
Qy      481 RDRYWRDLQAKLQATTSGRWATELPMWGCMAHNSGALF 520
Db      406 RDRYWRDLQAKLQATTSGRWATELPMWGCMAHNSGALF 445

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RESULT 7

```

US-09-950-510-23
; Sequence 23, Application US/09950510
; Patent No. 6740514
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy
; TITLE OF INVENTION: 46798, A No. 6740514el Human Matrix Metalloproteinase And Uses Th
; FILE REFERENCE: 10147-4501
; CURRENT APPLICATION NUMBER: US/09/950,510
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/251,156
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-510-23

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Query Match      77.9%; Score 2207; DB 4; Length 469;
Best Local Similarity 87.5%; Pred. No. 2,2e-211;
Matches 420; Conservative 4; Mismatches 34; Indels 22; Gaps 5;

Qy      52 KAPTSTFSDAIRAFQWVSQLPVSGVLDRAITLROMTRPCGVTDITNSYAAMERISDLFA 111
Db      1 KAPTSTFSDAIRAFQWVSQLPVSGVLDRAITLROMTRPCGVTDITNSYAAMERISDLFA 60
Qy      112 RRRTRKRRKRRKPAKQGNKWKYKQHLSTYLVNMPHEHLRSRQFGAPCAPSSCGATS---QRW 168
Db      61 RRRTRKRRKRRKPAKQGNKWKYKQHLSTYLVNMPHEHL-----PEPAVRGAVALAAQOLW 111
Qy      169 S--SGRPOPQAPLVTSGSPS-----KGTITMGAMPIMAGAPWRTPFLPRGSAHFDD 220
Db      112 SNVSLLEWEAHPAT--GPADIRLTLTFQGDHNDGLGNAPDGGALAHAFLEPRGSAHFDD 169
Qy      221 DERWLSRRGRNLFVTLAHEIGTILGLTHSPAPRALMAPYKRLGRDALISWDVLAQV 280
Db      170 DERWLSRRGRNLFVTLAHEIGTILGLTHSPAPRALMAPYKRLGRDALISWDVLAQV 229
Qy      281 SLYKPRPLGGSVAVALPGKLFDTFETWDSYSPQGRRPETQGPKYCHSSFDAITVDROOQLY 340

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Db      230 SLYKPRPLGGSVAVALPGKLFDTFETWDSYSPQGRRPETQGPKYCHSSFDAITVDROOQLY 289
Qy      341 IFKGSHEWEVAADGANVSEPRPLQERWVGLPNTIEAAVALNDGDFYFKGRCMRFRGPK 400
Db      290 IFKGSHEWEVAADGANVSEPRPLQERWVGLPNTIEAAVALNDGDFYFKGRCMRFRGPK 349
Qy      401 PYWGLPOLCRAGGLPRHPDAALFEPPLRLILFKGARYYVLARGGLQVEPYPRSLQDWG 460
Db      350 PYWGLPOLCRAGGLPRHPDAALFEPPLRLILFKGARYYVLARGGLQVEPYPRSLQDWG 409
Qy      461 GIPREVSGALPREDSITFFRDDRWRDLQAKLQATTSGRWATELPMWGCMAHNSGALF 520
Db      410 GIPREVSGALPREDSITFFRDDRWRDLQAKLQATTSGRWATELPMWGCMAHNSGALF 469

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RESULT 8

```

US-09-950-510-22
; Sequence 22, Application US/09950510
; Patent No. 6740514
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy
; TITLE OF INVENTION: 46798, A No. 6740514el Human Matrix Metalloproteinase And Uses Th
; FILE REFERENCE: 10147-4501
; CURRENT APPLICATION NUMBER: US/09/950,510
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/251,156
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-510-22

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Query Match      61.1%; Score 1731; DB 4; Length 393;
Best Local Similarity 85.2%; Pred. No. 5.3e-164;
Matches 341; Conservative 4; Mismatches 33; Indels 22; Gaps 5;

Qy      1 MVARVGLLRLALQULLMGLHDAQPAERGGQELKKEKAFLEKGYINEQVPAKPTSTFSS 60
Db      1 MVARVGLLRLALQULLMGLHDAQPAERGGQELKKEKAFLEKGYINEQVPAKPTSTFSS 60
Qy      61 DAIRAFQWVSQLPVSGVLDRAITLROMTRPCGVTDITNSYAAMERISDLFARRHTKMRK 120
Db      61 DAIRAFQWVSQLPVSGVLDRAITLROMTRPCGVTDITNSYAAMERISDLFARRHTKMRK 120
Qy      121 KRPAKQGNKWKYKQHLSTYLVNMPHEHLRSRQFGAPCAPSSCGATS---QRW--SGRPOP 175
Db      121 KRPAKQGNKWKYKQHLSTYLVNMPHEHL-----PEPAVRGAVALAAQOLW 171
Qy      176 QAPLVTSGSPS-----KGTITMGAMPIMAGAPWRTPFLPRGSAHFDDERWLSRR 229
Db      172 EAPAT--GPADIRLTLTFQGDHNDGLGNAPDGGALAHAFLEPRGSAHFDDERWLSRR 229
Qy      230 RGNLFLVTLAHEIGTILGLTHSPAPRALMAPYKRLGRDALISWDVLAQVSLYKPRPLG 289
Db      230 RGNLFLVTLAHEIGTILGLTHSPAPRALMAPYKRLGRDALISWDVLAQVSLYKPRPLG 289
Qy      290 SVAVOLPGKLFDTFETWDSYSPQGRRPETQGPKYCHSSFDAITVDROOQLYIFKGSHEWE 349
Db      290 SVAVOLPGKLFDTFETWDSYSPQGRRPETQGPKYCHSSFDAITVDROOQLYIFKGSHEWE 349
Qy      350 VAADGANVSEPRPLQERWVGLPNTIEAAVALNDGDFYFKP 389
Db      350 VAADGANVSEPRPLQERWVGLPNTIEAAVALNDGDFYFKP 389

RESULT 9
US-09-171-545-1
; Sequence 1, Application US/09171545
; Patent No. 656116

```


QY 24 PARRGGQELERKAAE-FLKXGYLNEQVPAKPTSTFRED---AIRAQWMSQLPVSGLVD 79
 Db 23 PEE-----KEAVDYTLLOGYLOKPLEGA-DDFRLEDITEALRTPOEASELFPVSGMD 74
 QY 80 RATTLRQMTPRRCGVTDITNSVYAAWAMERISDLFARHRTKMRKRKREPAKQGNKYVCOHLSYRL 139
 Db 75 DATRARMKQPRCGLEDPFN-----QKTLKULLIGH-WRKKHLTFRI 114
 QY 140 VNMPEHLASRQPGAFCAPPSSCGATSGRWSSGRPOPAPLTSSGSPSSKGTYYMGWA-MPL 198
 Db 115 LNVPSSTL-----SPSRVRAALHQAfKXYSN-----VAPLTFREVKA-----GMADIRL 157
 QY 199 MAQGPMPRTPF-----LPRRGEAHFPQDERMWSLSRRRGHNLFWVLAAHEI 242
 Db 158 SFHGR--QSPfCSNSFDQPGKVLAAHADVPBELGSVHFNDDEFWTEGYOQVNLHIAHEV 215
 QY 243 GHTGLTSPAPRALMAFYRKLRLGRDALLSMDVLAVOSLYGKPLGSSVAVQLPGLKFTD 302
 Db 216 GHALGLGHSRYTQALLMAFVAVGYQPYRPLHDDVAVGfQALYXK----- 258
 QY 303 FETMDSYSPQGRRETQG-----PRYCHSSFDALTVDHQOQLYTF 342
 Db 259 -----RRPEPDEEBEEVEEMHTVTSVTYTKPSMPNPSCSEVDAMMLGPRKTYAV 307
 QY 343 KGSHFWEVYAADGNVSEPRPL--QERWVGLPPTNEAAVSLNDGDFYFFFGGRCMFRGP 399
 Db 308 KGDVWVYTTDGS---RGLPRVSALBEGRLGNIDAAVYSPRTQTHFFFGKNTWRYVDF 363
 QY 400 KPVWGLPOLCRAGGLPRHPDAALEFPPLRLRLILFKGARVY---VLARGGHQVEPPYPRSL 456
 Db 364 KLSGPFPM--KLNVPEPRLDALVWPVNOQVPLFKSSGVWQWMLRTRDLS---RfPKXI 418
 QY 457 OD-WGCIPEBVSGLPRPDGSIIFRQDRKWRILDQATLQATTSGRNATELPMWGC 510
 Db 419 KELTPGVDPDPSAAMSWQDQVYFFKCKEYWRINQOLRVAKGYPRWYTH--WMHC 471

RESULT 12
 US-09-000-041A-2
 Sequence 2, Application US/09000041A
 Patent No. 6191255
 GENERAL INFORMATION:
 APPLICANT: Motoharu SEIKI et al.
 TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 STREET: 2033 K Street, N.W., Suite 800
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/000,041A
 FILING DATE: January 13, 1998
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP96/01956
 FILING DATE: July 12, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee Cheng
 REGISTRATION NUMBER: 40,949
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-721-8200
 TELEFAX: 202-721-8250
 TELEX:

```

1  INFORMATION FOR SEQ ID NO: 2 :
2  SEQUENCE CHARACTERISTICS:
3  LENGTH: 607
4  TYPE: Amino acid
5  STRANDEDNESS: Single
6  TOPOLOGY: Linear
7  MOLECULE TYPE: Protein
8  ORIGINAL SOURCE:
9  ORGANISM: Human
10 US-09-000-041A-2

Query Match
Best Local Similarity 18.9%; Score 535.5; DB 3; Length 607;
Matches 158; Conservative 84; Mismatches 216; Indels 93; Gaps 22;

QY 12 LQLLIMGLHDAQPERGSGELRKAEAFLEKYGVLNQVKAPSTFS-----DA 62
DB 23 LQTLIM----ILCATVCGTEQYFNEVEAWLQKTYL-----PTDDPMSTLRSAETWQA 72
QY 63 IRAPOWVSQLPVSGVLDRATLRCQTRRCQGVDTNSYAAMERISDLFARHTQMR-RKK 121
DB 73 LAAMQOFGVIMWTGKVDNRNTIDMWKKRCQVPO-----TGSSKFKHRRK 118
QY 122 RFAQGNKNTYQCHLSYLVN-----PEHLRS--RQFGAPCAPSSCGATSGRMSSGRP 173
DB 119 RYALTLGQWQKHLLTYSIKVTPEKVDPETRKAIIRAFDV-----MQNVTP 164
QY 174 -----QPAPLTSGSPESKGTFTW-----GMAPMLAQGAPWRTPLFLR---RGEAHFQ 220
DB 165 LTFEEVPSYLENKKRVDITIIIFASGFHGDSSPDEGGFLAHAYFPGEGIGDTHFDS 224
QY 221 DERKSLG--RRRGNLFFVLAHEIGHTLGLTHSPAPRALMAPYKLGDAL-LSMDVYL 277
DB 225 DEPTLTNPNDHGNDLFLVAHEIGHALGLEHSNDPLAIWAPFYQWETDNPGLPDDLQ 284
QY 278 AVQSLYQ----KPLGGSVAVOLPGKLFDTFETWDSYSPQGRPRPQGRY-----CH 325
DB 285 GIQKLYPEPDKIPPTPTPELPVPPHNSIPAPDRKNDKRPPEPPPTGRSPYQAKPNICD 344
QY 326 SSFPAITVDRQOOLYIFKGSHEWEVADGVNSSEPLQER--WVGSLPNIEAAVSLNDG 383
DB 345 GNFTTLAILR-REMFVFKDQMFWRV-RNNRVMDGYPMQLTFFMRGLPESIDAVYEN-SIG 401
QY 384 DFFPEKGRGCMRRGRGPRVWGLPQ--LCRAAGLPRHP-DALFFPPLRLILFKGARVYV 440
DB 402 NFFVEKKNKTVWRDITTLQPGYPHDLITGSGIPRPGISALIMWEDVGVGTFFFKGRVYR 461
QY 441 IARGGLQVEEYPRSLDWMGIPBEVSGA-LPRDSILFFPDDRYWRDQAKLTATISG 499
DB 462 YSEEMKTMGDGYPKPLITWKGIPESIQGAFVHKENGFTFYFKGKEYWKNFNQILKVEPGH 521
QY 500 RMATELPMWGC 510
DB 522 PRSLDPMWGC 532

RESULT 13
US-09-734-002-2
Sequence 2, Application US/09734002
Patent No. 6780412
GENERAL INFORMATION:
APPLICANT: Mochanu SEIKI et al.
TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSES: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

```

```
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,002
FILING DATE: 12-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/01956
FILING DATE: July 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 607
TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Protein
ORIGINAL SOURCE:
ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-734-002-2
```

```
Query Match 18.9%; Score 535.5; DB 4; Length 607;
Best Local Similarity 28.7%; Pred. No. 2,2e-44;
Matches 158; Conservative 84; Mismatches 216; Indels 93; Gaps 22;
```

```
12 LQLLIWHLDQAPRGGQELRKEAFLKGYLINEOVPRKPTSTRS-----DA 62
23 LQTLIM-----ILCATVCGTEQYFNVEWVLOKGYL-----PPTDPRMSVLSAETMOSA 72
63 IRAPQWSOLPVSGVLDATLROMTRPRCGVTDNYSYAMAMERISDLFARHRTKMR-RKK 121
73 LAAMQOFGYINNTGVNDRTIDMKKPRCGVDPDQ-----TRGSSKHIRK 118
122 RPAKQGNKYKQHLISYRLVNW-----PEHLRS--ROFGAPCAPSSCGATSORWSSGR 173
119 RYALTGQKQKHGHITYSIKNTVPRKGDPETRKAIKRAFDV-----WQNTVP 164
174 -----QPAAPLTSSGSSSKGTTM-----GWAMPMAQGAFWRTPLPR--RGAHPDQ 220
165 LTFEEVPSYLENGKRDVDITIIIFASGFHGDSSPFDGSGFLAHAYFFPGPGIGDTHFDS 224
221 DERMSLS--RRGRULFVVLAEIGHTGLTSPAPRALMAFYKRLGSDAL-LSMDPVL 277
225 DEPWTLGNPNHNDGDLFLVAVHELGHALGLEHNSNDPTAIMAFYQYMETDNFKLPRDDIQ 284
278 AVQSLYG-----KPLGSAVAQVLPGLFTDFETWDSYSPQGRRPETGPKY-----CH 325
265 GIQKIYGPDKIPPRPRPLPYVPRHSITPRADPRKNDKPRPRPRPGRSYSGAKENICD 344
336 SFPDAITVDROQOLYIFKGSHPWEVAADGNVSEPRPLQGR--WGLPRNIEAVALSNDG 383
345 GNFTLATILR-REMFVFKDQWFRVY-RNNRVMDGYVMQITVFWRGLPISIDAVYER-SDG 401
384 DYFFPRGACRFRGKPYWGLPQ--LCAAGLPRPR-DAALEFPPLRLILFKCARVYV 440
402 NFVFFPGNKYWFKDTTLQPGYPHDILITLSSGIPRPGIDSAIMWEDVGTFFGKGGRYR 461
441 IARGGLQVEPYPRSLQDWGCIPEEVSQA-LPRPDOSIIFPRDDRYWRDLQAKLQATISG 499
462 YSEEMKTMPPGYPKPTTWKGIPEBQGAFLVHKENGFYFYKQKEVWKKNQDLKAYEPH 521
500 RWATELPMWGC 510
522 PRSILKDFMGC 532
DB
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RESULT 14
US-09-211-704A-10
Sequence 10, Application US/09211704A
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Patent No. 6271014
GENERAL INFORMATION:
APPLICANT: de Saint-Vin, Blandine Marie
APPLICANT: Fossiez, Francois
APPLICANT: Caux, Christophe
APPLICANT: Leboucq, Serge J.E.
TITLE OF INVENTION: Mamalian Proteinases; Related Reagents
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,704A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/005,263
FILING DATE: 09-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF0781K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-211-704A-10
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Query Match 18.9%; Score 534.5; DB 3; Length 607;
Best Local Similarity 28.7%; Pred. No. 2,8e-44;
Matches 158; Conservative 84; Mismatches 216; Indels 93; Gaps 22;
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12 LQLLIWHLDQAPRGGQELRKEAFLKGYLINEOVPRKPTSTRS-----DA 62
23 LQTLIM-----ILCATVCGTEQYFNVEWVLOKGYL-----PPTDPRMSVLSAETMOSA 72
63 IRAPQWSOLPVSGVLDATLROMTRPRCGVTDNYSYAMAMERISDLFARHRTKMR-RKK 121
73 LAAMQOFGYINNTGVNDRTIDMKKPRCGVDPDQ-----TRGSSKHIRK 118
122 RPAKQGNKYKQHLISYRLVNW-----PEHLRS--ROFGAPCAPSSCGATSORWSSGR 173
119 RYALTGQKQKHGHITYSIKNTVPRKGDPETRKAIKRAFDV-----WQNTVP 164
174 -----QPAAPLTSSGSSSKGTTM-----GWAMPMAQGAFWRTPLPR--RGAHPDQ 220
165 LTFEEVPSYLENGKRDVDITIIIFASGFHGDSSPFDGSGFLAHAYFFPGPGIGDTHFDS 224
221 DERMSLS--RRGRULFVVLAEIGHTGLTSPAPRALMAFYKRLGSDAL-LSMDPVL 277
225 DEPWTLGNPNHNDGDLFLVAVHELGHALGLEHNSNDPTAIMAFYQYMETDNFKLPRDDIQ 284
DB
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QY 278 AVOSLYG-----KPLGSSVAVOLPGKLFDTFETMDSVPGGRPEYOGPKY-----CH 325
 Db 285 GIGKXIGPPDKXIPPPRPPLPFTVPKHSIPADPRKDRPPRPPTGRBSPGAKPNICD 344
 QY 326 SSGDALTVDROOQLYIFKSGHFEVADGNVSEPRLOER--WVGLPNIEAAVSLNG 383
 Db 345 GNETLAIIR-REMFVFKDQMFWRV-RNNRVMDGYMQITTFYRGLEPSIDAVYEN-SDG 401
 QY 384 DFFFFKGRGWRPRGPKVWGLPQ--LCRAAGLPRHP-DALFFPPLRLILFKGARYYV 440
 Db 402 NVVFFKGNKYWPKDITTLQPGYPHDILITGSGIPPHIGIDSAIWMEDVGKTFYFKEDRYR 461
 QY 441 IARGLOVPPYPRSLQDWGIPPEVSGA-LPRPOSSIFFRDDRYRLDQAKLQATTSG 499
 Db 462 YSEEMKTMDPGYPKPIITWKGIPESBQGFVHKENGFTYFKGKEXKFNQILKVERGY 521
 QY 500 RWATELPMWGC 510
 Db 522 PRSLIKDFMGC 532

RESULT 15

US-08-704-711A-3
 ; Sequence 3, Application US/08704711A
 ; Patent No. 6114159
 ; GENERAL INFORMATION:
 ; APPLICANT: WILL, Horst
 ; APPLICANT: HINZMANN, Bernd
 ; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/704, 711A
 ; FILING DATE: 20-NOV-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/DE95/00357
 ; FILING DATE: 17-MAR-1995
 ; PRIOR APPLICATION NUMBER: DE 4438838.1
 ; FILING DATE: 21-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE 4409663.1
 ; FILING DATE: 17-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GRANADOS, Patricia D.
 ; REGISTRATION NUMBER: 33,683
 ; REFERENCE/DOCKET NUMBER: 26083/124
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 672-5300
 ; TELEFAX: (202) 672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 669 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-704-711A-3

Query Match 18.8%; Score 534; DB 3; Length 669;

Best Local Similarity 27.4%; Pred. No. 3.6e-44;
 Matches 167; Conservative 64; Mismatches 206; Indels 172; Gaps 21;
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 QY 64 RAQVNSQLPVSGVLDRAITLROMTRPRCGVTDITNSVAAWERISDLPAHRTKMRKRGF 123
 Db 84 AEMQRFYGIPTVGVLDERTKEMWKPRCGVD-----QPGRVK-----ANLRRRRKY 132
 QY 124 AKQGNKKWKHLSRLVNVMPHLRSROPGACAPSSCGATSORWSSGRPOQAPLTSGS 183
 Db 133 ALTRGKNNHLLTTSIQNYTEKL-----
 QY 184 PSSKQTTTMCW-----AMPLAQAAPRTTFLPRR----- 213
 Db 156 -----GWYHMEAVRRAFRVWEQHTPLVFQEVPEYEDIRLRROKADIMVLFAQGFH 206
 QY 214 -----GEAHPDODERSLSRR--RGRNLFVYLAHEIGHTLG 247
 Db 207 GDSPPFDGTGGLAHAYFPGPLGDTGTFDADEPMTSSTDHGNMLPLVAVHELGHALG 266
 QY 248 LTHSPAPRALMAPYKRLGRDAL-LSWDVYLAQSLYKPLG-----GSYAVOLPGK 298
 Db 267 LEHSSNPNAIMAPPYQMKDVNFKLPEDDLRGICQLYGTGPDGPQPTQPLPTVTPRRPGR 326
 QY 299 LFTDFETWDSYSPQ-----GRRETQPKCHSSPDATV 333
 Db 327 P-----DHRPRPPQPPPPGKPRPKPPGPPVPPRATERPDQYGPNCDDDFDTVM 379
 QY 334 DROOQLYIFKSGHFEVVAADGNVSE-PRPLOERWGLPNIEAAVSLNDGDFPFPGGR 392
 Db 380 LR-GEVFFVKGKWFVFRVHRNRVLDNYPMPDIGHFWRGLPQDI-SAAIERODGRFVFKGDR 437
 QY 393 CWRFGPKPVWGLPQ-LCAG--GLP-RHPDALFFPPLRLILFKGARYYVLAAGLQVE 449
 Db 438 YVLFREANLEPGYPOPLTSYGLIPYDRIDTAIWMPEPTGHTFFQEDRYRFRNEGTORD 497
 QY 450 FYPRSLQDWGIPPEVSGALPRPDGS-IIFFRDRYWRDLQAKLQATTSGRMATELPM 508
 Db 498 PGYPKPIVWQGIPLASPKGAFISNDAAATYTFYKGTIKWKFENRLEMRBEGYPSILRDFM 557
 QY 509 GCM-HANG 516
 Db 558 GQEHVERG 566

Search completed: June 13, 2005, 18:03:21
 Job time : 45 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2005, 07:28:01 / Search time 264 Seconds

(without alignments)
3222.969 Million cell updates/sec

Title: US-10-791-980-6
Perfect score: 2834
Sequence: 1 MVARGLLRALLQLLWGL.....WATLPMWCMHANGSALF 520

Scoring table: BIOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QFMT=fastcap -SUFFIX=rml -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPM=prco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10791980 @CGN 1.1 177 @runat_13062005_104719_19951 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Issued Patents NA:*
- 2: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCUTUS.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2834	100.0	1597	4	US-09-862-631-3
2	2792	98.5	1560	4	US-09-950-510-3
3	2792	98.5	2527	4	US-09-950-510-1
4	2764	97.5	2275	3	US-09-391-104-1
5	2324.5	82.0	1335	4	US-09-950-510-13
6	2324.5	82.0	2310	4	US-09-950-510-11
7	602	21.2	3530	3	US-08-704-711A-10
8	602	21.2	3530	3	US-09-521-220-10
9	575	20.3	1524	4	US-09-171-545-7
10	575	20.3	2264	4	US-09-171-545-22
11	560	19.8	2049	4	US-09-171-545-23
12	555	19.6	3437	3	US-08-704-711A-9

13	555	19.6	3437	3	US-09-521-220-9	Sequence 9, Appli
14	555	19.6	3437	3	US-09-919-497-34	Sequence 34, Appli
15	554	19.5	3403	4	US-08-448-489-2	Sequence 2, Appli
16	554	19.5	3403	4	US-09-689-730-2	Sequence 1, Appli
17	551	19.4	1923	3	US-09-294-841-1	Sequence 8, Appli
18	550	19.4	1521	4	US-01-171-545-8	Sequence 1, Appli
19	538.5	19.0	2116	3	US-09-000-041A-1	Sequence 1, Appli
20	538.5	19.0	2116	3	US-09-734-002-1	Sequence 2392, Ap
21	515	18.2	2666	4	US-09-949-016-2392	Sequence 2393, Ap
22	515	18.2	2666	4	US-09-949-016-2393	Sequence 3, Appli
23	515	18.2	3691	3	US-08-704-711A-3	Sequence 8, Appli
24	513.5	18.1	3456	3	US-09-521-220-8	Sequence 8, Appli
25	513.5	18.1	3456	3	US-09-521-220-8	Sequence 1, Appli
26	506.5	17.9	3695	3	US-09-211-704A-1	Sequence 124, App
27	492.5	17.4	2177	4	US-09-919-016-124	Sequence 9, Appli
28	478	16.9	1233	4	US-09-171-545-9	Sequence 10, Appli
29	478	16.9	1233	4	US-09-171-545-10	Sequence 4937, Ap
30	476.5	16.8	2248	4	US-09-949-016-4937	Sequence 1410, Ap
31	476.5	16.8	2247	4	US-09-023-655-1410	Sequence 1, Appli
32	476.5	16.8	2256	1	US-07-794-393-1	Sequence 1, Appli
33	476.5	16.8	2256	1	US-08-001-711-1	Sequence 3, Appli
34	473	16.7	2260	1	US-07-794-393-3	Sequence 3, Appli
35	473	16.7	2260	1	US-08-001-711-3	Sequence 11, Appli
36	456	16.1	1257	4	US-09-171-545-11	Sequence 18, Appli
37	456	16.1	1272	4	US-09-171-545-12	Sequence 8, Appli
38	427.5	15.1	1521	4	US-08-994-689C-18	Sequence 4689, Ap
39	427.5	15.1	2792	4	US-08-994-689C-8	Sequence 12, Appli
40	426.5	15.0	2717	1	US-09-949-016-4689	Sequence 1264, Ap
41	425.5	15.0	1717	1	US-08-228-515A-12	Sequence 5094, Ap
42	425.5	15.0	1717	1	US-08-645-885-12	Sequence 352, App
43	403	14.2	1970	4	US-09-023-655-1264	
44	403	14.2	1970	4	US-09-949-016-5004	
45	403	14.2	1973	4	US-09-949-016-352	

ALIGNMENTS

RESULT 1
US-09-862-631-3
; Sequence 3, Application US/09862631
; Parent No. 6734005
; GENERAL INFORMATION:
; APPLICANT: Holmgren, Erik
; APPLICANT: Kihlen, Mats
; APPLICANT: Wood, Tim
; APPLICANT: Ekblom, Jonas
; TITLE OF INVENTION: No. 6734005el Matrix Metalloproteinases
; FILE REFERENCE: 00014regUS
; CURRENT APPLICATION NUMBER: US/09/862,631
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 206119
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-862-631-3

Alignment Scores:
Pred. No.: 4.9e-226
Score: 2834.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0

US-10-791-980-6 (1-520) x US-09-862-631-3 (1-1597)

QY 1 MetValAlaArgValGlyValLeuLeuArgAlaLeuGlnLeuLeuTrrGlyHisIleu 20
DB 35 ATGTTCGGCGCGCTGCTGCTGCTGCTGCTGCGCCCTGCGAGCTGCTACTGTGTGGGCGACCTTG 94

QY	21	AspAlaGlnProAlaGluArgGlyGlyGlnGluMetValGlySerGluAlaGluAlaPheLeu	40
Db	95	GAGCGCCAGCCCGCGAGCGCGAGGGCCAGAGGCTGGCCAAAGAGCGCGAGGCAATTCCTA	154
QY	41	GluValPyrGlyTyrTyrLeuAsnGlnGlnAlaProIleValaPheProThrSerThrArgPheSer	60
Db	155	GAGAACTACGATACCTCAATGMAACAGATCCCAAGATCCCACTCCACTCGATGATACG	214
QY	61	AspAlaIleLeuAlaPheGlnTyrValSerGlnLeuProValSerGlyValLeuAspArg	80
Db	215	GATGCAATCAAGAGCTTTCAGTGGGGTGTCCAGCTACCTGTACAGCGCGCTTTCGACCC	274
QY	81	AlaThrLeuArgGlnMetThrArgProArgCysGlyValThrAspThrAsnSerTyrAla	100
Db	275	GCCACCCCTGGCCCGATACCTGCTCCCGCGCGGGGTTCAGATACCAACAGCTTATGGCG	334
QY	101	AlaTyrAlaGluArgIleSerAspLeuPheAlaArgIleArgThrIlePheMetArgGlyLe	120
Db	335	GCTCGGGCTGAGAGATCAGTGACTGTGTTGTGTACACCCGACCAAAATGAGGGCTTAAG	394
QY	121	LeuArgPheAlaValSerGlnGlyAsnValTyrTyrIleSerGlnIleSerTyrArgLeuVal	140
Db	395	AAAGCCCTTGCAAAAGCAAGGTAAACAAATGGTATCAAGAGACACTCTCTTAACGGCTGGTG	454
QY	141	AsnTyrProGlnIleAspArgSerArgGlnPheGlyValaProCysAlaProProSerSer	160
Db	455	AACTGGCTGAGCATCTCCGAGCGCGCAATTCGGGGCCCGTGGCGCCGCTTCCTCACT	514
QY	161	CysGlyAlaThrSerGlnArgTyrPheSerSerGlyValArgProGlnProGlnAlaProLeuThr	180
Db	515	TGTGAGCAACGTCTACGCGCTGAAGTCTCGGAGAGCCCAACCAAGGCTCCGCTGACA	574
QY	181	SerGlySerProSerSerIleGlyThrThrThrMetGlyTyrAlaMetProLeuMetAla	200
Db	575	TCCGGCTCACTCTTCCAAAGGGAGACAAACGATGGCTGGGCAATGCTTGTATGGCC	634
QY	201	GlnGlyAlaProTyrPheThrProPheLeuProArgArgGlyGluAlaHisPheAspGln	220
Db	635	CAGGGAGCGCCCTGGGGCAGCGCTTTCGCGCCCGCGGAGAGCCGACCTTGACCA	694
QY	221	AspGluArgTyrPheSerLeuSerIleArgArgGlyValArgAsnLeuPheValValLeuAlaHis	240
Db	695	GATGAGCGCTGGTCCCTGAGCCCGCGCGGGGCGCAACCTGTTGTGTGTCTGGCGCAC	754
QY	241	GluIleGlyHisThrLeuGlyLeuThrHisSerProAlaProArgAlaLeuMetAlaPro	260
Db	755	GAGATCGGTCAACCGCTTGGCTTCCACCTACGCGCGCGCGCGGCTCATGGGCCCC	814
QY	261	TyrTyrLeuValArgLeuGlyValArgAspAlaLeuLeuSerTyrPheAspValLeuAlaValGln	280
Db	815	TACTACAAAGAGGCTGGCGCGCGACCGGCTGTCACTGAGCGAGCAAGTGTGGCGCTGCAG	874
QY	281	SerLeuTyrGlyValSerProLeuGlyGlySerValaValaGlnLeuProGlyIlePhePhe	300
Db	875	ACCCTGTATGGGAAGCCCTTAGGGGGCTCAGTGGCCGTCCAGCTCCAGAAAGCTGTTC	934
QY	301	ThrAspPheGlnThrTyrAspSerTyrSerProGlnGlyArgArgProGluThrGlnGly	320
Db	935	ACTGACTTTGAGACTGTGGAGCTCTCCACAGCCCCCAAGAAAGCGCCCTGTAAAGCGAGGGC	994
QY	321	ProIleTyrCysHisSerSerPheAspAlaIleThrValAspArgGlnGlnLeuTyr	340
Db	995	CCTAAATCTCCACTCTTCTTGATGCCATCACTTAAACAGGCAACAGCAACTGTAC	1054
QY	341	IlePheValSerHisPheThrPheGlnValAlaAlaAspGlyAsnValSerGluProArg	360
Db	1055	ATTTTAAAGGAGCAATTTCTGGAGATGGACAGCTGATGGCAACGTTCAAGAGCCCGGT	1114
QY	361	ProLeuGlnGluArgTyrValGlyLeuProProAsnIleGlnAlaAlaValSerLeu	380
Db	1115	CCACTTGCAGGAAGATGGGTGGGGCTGCCCTCCCACTTGAAGGCTCGGACAGTGCATTTG	1174

QY	381	AenApbGlyAspPheTyrPhePheLysGlyIArgCystrPArgPheArgGlyProLys	400
Db	1175	AATGATGGAGATTCTACTTCTTCAAAAGGGGGTCAGTGTGAGAGTTCCGGGGCCCAAG	123
QY	401	ProValTrrGlyLeuProGlnLeuCybArgAlaGlyGlyLeuProArgHisProAspAla	420
Db	1235	CCAGTGTGGGGTCTCCACAGCTGTGCGGGAGGGGGCTGGCCCCGCCATCTCAGCGC	129
QY	421	AlaLeuPhePheProProLeuArgArgLeuIleLeuPheLysGlyAlaArgTyrTyrVal	440
Db	1295	GCCCTCTTCTCCCTCCTCTGGCGCCGCATCCTTTCMAAGGTGCCCGCTACTACGTG	135
QY	441	LeuAlaArgGlyGlyLeuGlnValGluProTyrTyrProArgSerLeuGlnAspTrpGly	460
Db	1355	CTGGCCCCGAGGGGAGCTCAAGATGGAGCCACTACCCCGAAGCTCTCAGACTGGGGA	141
QY	461	GlyIleProGlnGluValSerGlyValAlaLeuProArgProAspGlySerTlleIlePhePhe	480
Db	1415	GGCATCCCTGAGAGAGCTAGCGGCCCTTCGCCAGGCCCGAAGGTCTCATATCTTCTTC	147
QY	481	ArgAspAspArgTyrTrrPArgLeuAspGlnAlaLysLeuGlnAlaIrrThrSerGlyArg	500
Db	1475	CGAGATGACCCCTACTGTGGCGCTCGACACGGCCAAATCGCAGGCAACCACTGGGGCCGC	153
QY	501	TrrAlaThrGluLeuProTrrMetGlyCysThrPheIleAlanserGlySerAlaLeuPhe	520
Db	1535	TGGGCGACCGAGCTGCCCTGATGAGGCTGCTGGCGATCCCAACTCGGGAGACGCCCTGTCTC	159

RESULT 2

US-09-950-510-3
; Sequence 3, Application US/09950510

; Patent No. 6740514
; GENERAL INFORMATION:

APPLICANT: Curtis, Rory
TITLE OF INVENTION: 45706

FILE REFERENCE: 10147-45U1

CURRENT FILING DATE: 2001-09-10

;
PRIOR APPLICATION NUMBER: 60/251,156
;
PRIOR FILING DATE: 2000-09-08
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; NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 3
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; LENGTH: 1560

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/ LENGTH: 1560
; TYPE: DNA

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US-09-950-510-3
ORGANISM: Homo sapiens

Alignment Scores:

Pred. No.: 1,
Score: 27

Percent Similarity: 99

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perc local similarity: 99
Query Match: 98

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DB: 4

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Db 1 ATGTCGCGCGC

Qy 21 AspalaginPro

61 GACGCGCAAGCCCG

D_B

41 01/01/2024

[illegible]

DD 121 GAGAGTACGGAT

61 Aspaialearga

Db 181 GATGCCATCAGAG

Alignment Scores:			
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Score:	2,792.00	Matches:	519
Percent Similarity:	99.62%	Conservative:	0
Best Local Similarity:	99.62%	Mismatches:	1
Query Match:	98.52%	Indels:	2
DB:	4	Gaps:	0

US-10-791-980-6 (1-520) x US-09-950-510-3 (1-1560)	
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Db	1 ARGTCGGCGCGGCTCGCTCTCTCGCGGCCCTCGACAGTGCCTACTGTGGGGCCACTG 60
QY	21 AspAlaGlnProAlaGlnArgGlyGlyGlnLeuLeuArgGlyGlnAlaGlnAlaPheLeu 40
Db	61 GACGGCCGAGCCCGCGAGCCGAGAGCCAGAGCTGGGCAAGAGGAGGCGGACATTCCTA 120
QY	41 GlyIleYrGlyYrLeuAsnGluGlnValProIleValaProThrSerThrArgPheSer 60
Db	121 GAGAAGTACGATACCTCAATGAACAGGTCCCAAACTCCCAACTCCATCCGATTACG 180
QY	61 AspAlaIleArgAlaPheGlnTrpValSerGlnLeuProValSerGlyValLeuAspArg 80
Db	181 GATGCATACAGAGCTTTCATGTGGGTCTCCACAGTACTCTTACGCGCGCTGTGGACCG 240

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QY      81 AAlthLeuArgGlnMetThrArgProArgCyGylValThrAspThrAsnSerTyraIa 100
DB      241 GCCACCTCGCGCAGATGACTGCTCCCGCTGGCGGGATTACAGATACCAACGTTATGGC 300
QY      101 AAlTPrAlAGlUArgGllSeSerAspLeuPheAlaArgHlaArgThlylMetArgGlyV 120
DB      301 GCTGGGCTGAGAGGATGAGTCACTGTTGCTAGACACCGGACCAAAATGAGGCTTAAG 360
QY      121 LysArgPheAlaLysArgGlnGlyAsnLysTyPTrLysGlnHlaLeuSerTyraArgLeuVal 140
DB      361 AAACGCTTGGCAAGAGATACAAATGGTACACAGACACTTCTCTACCGCTGAGT 420
QY      141 AsnTPrProGlnHlaLeu-ArgSerArgGlnPheGylValAProCyAlaAProProSeSe 160
DB      421 AACTGGCTGAGATCTGCGCGAGCGGACGTTCCGGGGCGCGGTGGCGCGCTTCAG 480
QY      160 rCyGylValAlthrSerGlnArgTrpSerSerGylValTrpProGlnProGlnAlaProLeuTh 180
DB      481 TTGTGGAGCAAGCTCTCAGCGCTGAGGTTCTGGAGAGCCCAAGCCACAGGCCCTGAC 540
QY      180 rSerGylSerProSerSerSerGylYThrLThrThrMetGlyTrpAlaMetProLeuMetAl 200
DB      541 ATCCGGCTCACTTCTTCCAGGGAGCCACACAGATGGGCTGGGCAATGCTTTGATGGC 600
QY      200 aGlnGylAlaProTPrArgThrProPheLeuProArgArgGylValAlaHlaIAspPheArg 220
DB      601 CCAGGGGGGGCCCTGGCGCAGCGCTTC-CGCGCCCGCGCGGAGAGCCGACCTTGACCA 659
QY      220 nAArgLysArgTrpSerLeuSerArgArgArgGylValArgAsnLeuPheValValLeuAlaH 240
DB      660 AAGATGAGCGCTGGTCCCTAGCGCGCGCGCGCGCCCAACCTGTTGTGTGTGTGCGCGA 719
QY      240 aGlnLysGlnHlaIAspThrLeuGlyLeuThHlaIAspProAlaProArgAlaLeuMetAlPr 260
DB      720 CCAAGATCGGTCACACGCTTGAGCTCACCACCTGCGCGCGCGCGGCTCATGGCGGC 779
QY      260 rTyTrTyLysArgLeuGylValArgAspAlaLeuLeuSerTrpAspArgValLeuAlaValG 280
DB      780 CTACTACAAAGAGGCTGGCGCGGCGCGCTGCTCACTGGAGAGAGTCTGGCCCTGCA 839
QY      280 nSerLeuTyrglyLysProLeuGlyGlySerValAlaValGlnLeuProGlyLysLeuTh 300
DB      840 GAGCGCTGTAGGAGAGCCCTAGGGGCTCAGTGGCGCTCCAGCTCCAGGAAAGCTGT 899
QY      300 ePhrAspPheGlnThrTrpAspSerTySerProGlnGlyArgArgProGlnThrGlnH 320
DB      900 CACTGACTTTGAGACTGGGACTCTTACAGCCCCCAAGAGGCGCCCTGAAACGCGAG 959
QY      320 YProLysTyCyWHlaSeSerSerPheAspAlaIleThrValAspArgGlnGlnLeuTy 340
DB      960 CCTTAATACTGCACTCTTCTTGATGCACTCATGTAGACAGGCAACAGCAATGTA 1019
QY      340 rLLePheLysGlySerHlaPheTrpGlyValAlaAlaAspGlyAsnValSerGlnProAr 360
DB      1020 CATTTTAAAGGAGCATTCTTGGGAGGTGGCAGCTGATGGCAAGTCTCAGAGCCCG 1079
QY      360 gProLeuGlnGlyArgTrpValGlyLeuProProAsnLysGlnAlaAlaValSerSe 380
DB      1080 TCACACTGCAAGAAAGTGGGTGGGCTGCCCCCAACATTGAGGCTGGCGCAGTGCATT 1139
QY      380 uAsnAspGlyAspPheTyPhePheLysGlyGlyArgCyBTrpArgPheArgGlyProLy 400
DB      1140 GAATATGAGATTTTACTTCTTCAAGGGGATGCAATGCTGAGGTTCCGGGGCCCCCA 1199
QY      400 aProValITrpglyLeuProGlnLeuCyAlaArgAlaGlyGlyLeuProArgHlaProAspAl 420
DB      1200 GCCAGTGTGGGTCTCCCAAGCTGTGGCGGAGCGGCGCTGCCCCGCAATCTGACCC 1259
QY      420 aAlaLeuPhePheProProLeuArgArgLeuLleuPheLysGlyValaArgTyTrTyra 440
DB      1260 CGCCCTCTTCTCTCTCTGCGCGCGCTCATCTTCAAGGAGTCCGCGCTACTACGT 1319

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QY      440 lLeuAlaArgGlyGlyLeuGlnValGlnProTyTrpProArgSerLeuGlnAspTrpG 460
DB      1320 GCTGGCCCGAGGGGAGCTGCAAGTAGAGCCCTTACTTACCCCGCAAGCTGCAAGACTGGGG 1379
QY      460 YGlyLysProGlnGlnValSerGlyValaLeuProArgProAspGlySerLleIlePhePh 480
DB      1380 AGGCAATCCCTGAGAGGTACAGCGGCGCTGCGAGGCGCGATGGCTCATCATCTTCTT 1439
QY      480 eArgAspAspArgTyTrpArgLeuAspGlnAlaLysLeuGlnAlaThrThrSerGlyAr 500
DB      1440 CCGAGATGACCCCTTACTGCGCGCTGCAACAGGCCAAACTGCAAGCAACCACTCGGGCGG 1499
QY      500 gTrpAlaThrGlyLeuProTPrMetGlyCyBTrpHlaAlaAsnSerGlySerAlaLeuTh 520
DB      1500 CTGGGCCCAAGAGCTGCGCTGATGGGCTGTGGCATGCGCACTCGGGAGCGCCCTGT 1559
QY      520 e 520
DB      1560 C 1560

RESULT 3
US-09-950-510-1
; Sequence 1, Application US/09950510
; Patent No. 6740514
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory
; TITLE OF INVENTION: 46798, A No. 6740514el Human Matrix Metalloproteinase And Uses Th
; FILE REFERENCE: 10147-45U1
; CURRENT APPLICATION NUMBER: US/09/950,510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/251,156
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patencin version 3.0
; SEQ ID NO 1
; LENGTH: 2527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-950-510-1

Alignment Scores:
Pred. No.: 2,94e-222 Length: 2527
Score: 2792.00 Matches: 519
Percent Similarity: 99.62% Conservative: 0
Best Local Similarity: 98.52% Mismatches: 1
Query Match: 98.52% Indels: 2
DB: 4 Gaps: 0

US-10-791-980-6 (1-520) x US-09-950-510-1 (1-2527)
QY      1 MetValAlaArgValGlyLeuLeuLeuArgAlaLeuGlnLeuLeuLeuTrpGlyHlaLeu 20
DB      300 ATGTGTGGCGCGGTGGCTCTTGGTGGCGGCTTGCAGCTGTCTGTGGGGCCACCTGG 359
QY      21 AspAlaGlnProAlaGlnLysArgGlyGlyGlnLysLeuArgGlyValaGlnLlaPheLeu 40
DB      360 GACGCCAGCCCGCGGAGGCGGAGGCGCAGAGCTGCCGAAGAGCGGAGGCAATTCCTTA 419
QY      41 GlnLysTyTrgLyLysLeuAsnGlnGlnValProLyAlaAProThSerThrArgPheSer 60
DB      420 GAGAAGTACGATACCTCAATGACAGGTCGCCAAAGCTCCCACTGCCACTGATTCAGC 479
QY      61 AspAlaLysArgAlaPheGlnTrpValSerGlnLeuProValSerGlyValLeuAspArg 80
DB      480 GATGCAATCAGAGCGTTTCAAGTGGATGCCAGCTTCTGTCAAGCGCGGTGGACCC 539
QY      81 AAlthLeuArgGlnMetThrArgProArgCyGylValThrAspThrAsnSerTyraIa 100
DB      540 GCCACCTCGCGCAGATGACTGCTCCCGCTGGGGTTACAGATACCAACAGTTATGGC 599
QY      101 AAlTPrAlAGlUArgGllSeSerAspLeuPheAlaArgHlaArgThlylMetArgGlyV 120
DB      600 GCTGGGCTGAGAGATGATGACTTGTGTTGCTTACACACCGGACCAAAATGAGGCGTAA 659

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406 AAACGCTTTGCAAGCAAGTGAACAATGTCACAGCAGCCTCTCTCAACGCGCTGGTG 465
QY 141 AentPrProgluHleu-ArgSerArgGlnPheGlyAlaProCyAlaProProSerSe 160
DB 466 AACTGGCCCTGAGCATCTGCGGAGCGGAGTTCGGGGGCGGTGGCCGCCCTTCCAG 525
QY 160 rCyGlyAlaIthrSerGlnArgTrpSerSerGlyArgProGlnProGlnAlaProLeuTh 180
DB 526 TTGTGAGACGACGTCTCAAGCGCTGAGATTCTGGAGAGCCCAAGCCCAAGCCCGCTGAC 585
QY 180 rSerGlySerProSerSerSerGlyThrThrThrMetGlyTrpAlaMetProLeuMetAl 200
DB 566 ATCCGCGCTACCTTCTTCAAGGGAGCAACAAGATGGGCTGGCAATCTCTTGAATGGC 645
QY 200 agInGlyAlaProTrpArgTrpPheLeuProArgArgGlyGlyAlaIlePheAspG 220
DB 646 CCAAGGGGGGCGCTGGCGGACCCCTTC-CTGCCCCCGCGCGGGAATTTACTTCAGCA 704
QY 220 rAspGlyArgTrpSerLeuSerArgArgArgGlyArgAsnLeuPheValIleuAlaH 240
DB 705 AGATGAGCGCTGCTGCTGAGCGCGCGCGGCGCAACTGTTCGTGTGCTGGCGCA 764
QY 240 gGlyIleGlyIleThrLeuGlyLeuThrIleSerProAlaProArgAlaLeuMetAlaP 260
DB 765 CGAGATCGGTCAACGCTTGGCTCAACCACTGCGCGCGCGCGCTCATGCGCGC 824
QY 260 CTATTrpIleArgLeuGlyArgAspAlaLeuLeuSerTrpAspAspValIleuAlaVal 280
DB 825 CTACTCAACAGAGCGCTGGCGCGGACCGCGCTGCTCACTGGAGAGAGCTGCGCTGCA 884
QY 280 nSerLeuTrpGlyIleArgProLeuGlyIleSerValAlaValGlnLeuProGlyIleVal 300
DB 885 GAGCGCTGATGGGAAGCCCTTACGAGGGGCTCAGTGGCGCTGCAAGCTCCAGAAAGCTGT 944
QY 300 eThrArgPheGlnIleThrTrpAspSerTrpSerProGlnGlyArgArgProGlnIle 320
DB 945 CACTACCTTGAAGACTGGAGCTCTCAAGCGCCCAAGAGAGCGCGCTGAAACGAGG 1004
QY 320 rProLeuTrpCyHleSerSerPheAspAlaIleThrValAspArgGlnGlnLeuTrp 340
DB 1005 CCTCAATATCTGCCACTCTTCTCGATGCCATCTGATGAGACAGGCAACAGCACTGTA 1064
QY 340 rIlePheIleGlySerSerIlePheTrpGlyAlaIleAspGlyAsnValSerGlnProAr 360
DB 1065 CATTTTAAAGGAGCAATTTCTGGAGGTGGCAGCTGATGGCAAGCTCTCAGAGCCCG 1124
QY 360 gProLeuGlnGlyIleGlyIleArgProAsnIleGlyAlaIleValIleSerIle 380
DB 1125 TCCACTGCAAGAAATGGGTGGCGTGGCCCAACATTTGAGGCTGGCGAGTGCATT 1184
QY 380 uAsnAspGlyAspPheTrpPhePheIleGlyIleArgCyHTrpArgPheArgGlyProly 400
DB 1185 GAATATGAGATTTCTACTTCTTCAAGGGAGTGCATCTGAGGTTCGGGGGCCCA 1244
QY 400 sProValTrpGlyLeuProGlnLeuCyHArgAlaGlyIleuProArgIleProAspAl 420
DB 1245 GCCAGTGGGGGTCTCCCAAGCTGGCGGAGGCGGCGTGGCCCGCATCTGAGCGC 1304
QY 420 AAlaLeuPhePheProProLeuArgArgLeuIleLeuPheIleGlyAlaIleArgTrpVal 440
DB 1305 CGCCCTCTTCTTCCCTCTGCGCGCTGCTCATCTTCAAGGGGTGGCGGCTGCTACTACT 1364
QY 440 lLeuAlaArgGlyIleuGlnValGlnProTrpTrpProArgSerLeuGlnAspTrpG 460
DB 1365 GCTGGCGCGAGGGAGCTCAAGTGGAGCCCTACTACCCCAAGTCTTCCAGAGACTGGGG 1424
QY 460 rGlyIleProGlnGlyIleuGlnValIleuProArgProAspGlySerIleIlePhePhe 480
DB 1425 AGGCATCTCTGAGAGGTCAAGCGCGCGCTGCGGAGCGCGCATGGCTCATCTTCTT 1484
QY 480 eArgArgAspArgTrpTrpArgLeuAspGlnAlaIleValLeuGlnAlaIleThrSerGlyArg 500
DB 1485 CCGAATGATACCGCTACTGGCGCTCGAACAGGCGCAAACTGACAGGCAACCACTCGGGCGG 1544

QY 500 gTrpAlaThrGlyLeuProTrpMetGlyCyHTrpIleAlaAsnSerGlySerAlaLeuTh 520
DB 1545 CTGGCGCAACCGAGCTGCGCTGATGGGTGCTGGCATGCGCACTCGGGAGCGCCTGT 1604
QY 520 e 520
DB 1605 C 1605
RESULT 5
US-09-950-510-13
; Sequence 13, Application US/09950510
; Patent No. 6740514
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory
; TITLE OF INVENTION: 46798, A No. 6740514el Human Matrix Metalloproteinase And Uses Th
; FILE REFERENCE: 10147-45U1
; CURRENT APPLICATION NUMBER: US/09/950,510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/251,156
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 13
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-950-510-13
Alignment Scores:
Pred. No.: 8,42e-184 Length: 1335
Score: 2324.50 Matches: 444
Percent Similarity: 85.22% Conservative: 0
Best Local Similarity: 85.22% Mismatches: 1
Query Match: 82.02% Indels: 77
DB: 4 Gaps: 1
US-10-791-980-6 (1-520) x US-09-950-510-13 (1-1335)
QY 1 MetValAlaArgValGlyLeuLeuLeuArgAlaLeuGlnLeuLeuLeuTrpGlyHleu 20
DB 1 ATGGTGGCGCGGTGGCTCTGCTGGCGCGCTGCGAGCTGCTACTGTGGGCGCACCTG 60
QY 21 AspAlaGlnProAlaGlnArgGlyIleGlnIleuArgIleValIleGlnAlaPheLeu 40
DB 61 GAGCGCCAGCGCGCGGAGGCGGAGGCGGAGAGCTGCCAAGAGAGCGGAGCATTCCTTA 120
QY 41 GlyIleTrpGlyTrpLeuAsnGlnGlnValProlyAlaIleProThrSerThrArgPheSer 60
DB 121 GAGAGTACGATACCTCAATGAACAGGTCCCAAGCTCCCACTCCACTGATTCAAC 180
QY 61 AspAlaIleArgAlaPheGlnTrpValSerGlnLeuProValSerGlyValLeuAspArg 80
DB 181 GATGCCATCAAGCGCTTCAAGTGGGTGTCCAGCTACTCTGTAAGCGGTGGTGAACCGC 240
QY 81 AlaThrLeuArgGlnMetThrArgProArgCyGlyValIleThrAspThrAsnSerTrpAla 100
DB 241 GCCACCTGCGCGCAATGATCTGCTCCCGCTCGGGGTTCAGATACCAACAGTTATGG 300
QY 101 AlaTrpAlaGlnArgIleSerAspLeuPheAlaArgHleArgTrpIleMetArgArgIle 120
DB 301 GCGTGGCGTGAAGGATCACTGATCTTGTTCCTAACAACCGGACCAAAATGAGCGGTAA 360
QY 121 LysArgPheAlaIleGlnGlyAsnIleTrpTrpIleValIleLeuSerTrpArgLeuVal 140
DB 361 AAACGCTTGGCAAG----- 375
QY 141 AentPrProgluHleuArgSerArgGlnPheGlyAlaProCyAlaProProSerSer 160
DB 375 ----- 375
QY 161 CyHAlaIleThrSerGlnArgTrpSerSerGlyArgProGlnProGlnAlaProLeuThr 180

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Db      375 -----
QY      181 SerGlySerProSerSerlySGlyThrThrThrMetGlyTyrPalamcProLeuMetAla 200
Db      375 -----
QY      201 Gln-GlyAlaProTTPArGThrProPheLeuProArGArglyGlyGlnAlaHisPheArgI 220
Db      376 CAAGGGGGGGCCCTGGCGCAGCCCTTC-CTGCCCCGGCGCCAGAGGCACTTCACCA 434
QY      220 nAaRGluArGTrpSerLeuSerArGArGlyArGAsnLeuPheValIleuAlaHis 240
Db      435 AGATGAGCCCTGCTGCTCGAGCGCGCGCGGCGGCAACCTGTCTGTGTGGCGCA 494
QY      240 eGluIleGlyHisGTrpLeuGlyLeuThrHisSerProAlaProArGAlaLeuMetAlaAr 260
Db      495 CGAGATCGGTCAACAGCTTGGCTCCACCACCTCGCCCGCGCGCGCTCACTGGCGCC 554
QY      260 cTyTyrIlysaArgLeuGlyArGAspAlaLeuLeuSerTTPAspAspValIleuAlaValG 280
Db      555 CTACTACAAAGAGCTGGGCGCGCAGCGCTGTCTACCTGGGAGCAGAGTGTGGCTGCA 614
QY      280 nSerLeuTyrGlyArGProLeuGlyGlySerValAlaValGlnLeuProGlyIlyLeuP 300
Db      615 GAGCTGTATGGAAAGCCCTAGGGGCTCAGTGGCGGTCCAGCTCCAGAAAGCTGTT 674
QY      300 eThAspPheGlyThrTTPAspSerTyrSerProGlnGlyArGArgProGlnThrGlnG 320
Db      675 CACTGACTTGGAGACCTGGGACTCTCAACGCCCCCAAGAGAGGCGCCCTGAAAGCAGCG 724
QY      320 YProLyTyTyCyHisSerSerPheAspAlaIleThrValAspArgGlnGlnLeuTy 340
Db      735 CCTAAATCTGCACTTCTCTGATGAGCCATCACTGTAGACAGGCAACGCAACTGTA 794
QY      340 rIlePheIlySGlySerHisPheTrpGlyValAlaAspGlyAsnValSerGluProAr 360
Db      795 CATTTTAAAGGAGCCCAATTCTGGAGCTGCAAGTGAAGTCCCAAGCTTCAAGCCCG 854
QY      360 gProLeuGlnGlnuArgTTPValGlyLeuProProAsnIleGlyValAlaValSerLe 380
Db      855 TCCACTGGCAGAAAGATGGAGTGGAGCTGCCCCCAACATGAGAGCTCGCGCACTGTCA 914
QY      380 uAsnAspGlyAspPheTyrPhePheIlySGlyGlyArGtyrTTPArgPheArgIlyPro 400
Db      915 GAAATGATGAAATTTCTACTTCTTCAAGGGGCTCAAGTGAAGTTCGGGGGCCCA 974
QY      400 sProValTTPGlyLeuProGlnLeuCyAsnArgIleGlyLeuProArGHisProAspAl 420
Db      975 GCCAGTGGGGGTCTCCACAGCTGTGCGGGGAGGGGCGTGGCCGCATCTGAGCC 1034
QY      420 aAlaLeuPhePheProProLeuArgArgLeuIleLeuPheIlySGlyValArgIlyTy 440
Db      1035 CGCCCTCTTCTCTCTCTCTGCGCGCTCATCTCTTCAAGGGTGGCCGCTACTAGT 1094
QY      440 lIleuAlaArgIlyGlyLeuGlnValGlnProCtyTyrProArgSerLeuGlnAspTTPG 460
Db      1095 GCTGGCGCGGAGGAGCTCAAGTGAAGCCCTACTACCCCGAAGTCTGCAAGAGCTGGGG 1154
QY      460 yGlyIleProGlnGlnValSerGlyAlaLeuProArgProAspGlySerIleIlePhe 480
Db      1155 AGGCATCTCTGAGAGGTCAAGCGCGCTCGAGGCGCGGAGGCTCCATCTTCTT 1214
QY      480 eArGAspAspArgIlyTTPArgLeuAspGlnAlaValLeuGlnAlaThrThrSerGlyAr 500
Db      1215 CCGAATAGACCGCTACTGCGCCCTCGACACAGGCCAACTGCAAGCAACCACTCGGGCG 1274
QY      500 gTTPAlaThrGlnLeuProTTPMetGlyCyArTPHisAlaAsnSerGlySerAlaLeuP 520
Db      1275 CTGGGCCACCGAGCTGCTGATGGGCTCTGTGCAATGCCAAGTGGGAGGCGCTCTGT 1334
QY      520 e 520
Db      1335 C 1335

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RESULT 6
US-09-950-510-11
/ Sequence 11, Application US/09950510
/ Patent No. 6740514
/ GENERAL INFORMATION:
/ APPLICANT: Curieis, Roy
/ TITLE OF INVENTION: 46798, A No. 6740514el Human Matrix Metalloproteinase And Uses T
/ FILE REFERENCE: 10147-45U1
/ CURRENT APPLICATION NUMBER: US/09/950,510
/ PRIOR APPLICATION NUMBER: 60/251,156
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 11
/ LENGTH: 2310
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-950-510-11

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Alignment Scores:

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Pred. No.: 1,86e-183 Length: 2210
Score: 2324.50 Matches: 44
Percent Similarity: 85.22% Conservative: 0
Best Local Similarity: 85.22% Mismatches: 1
Query Match: 82.02% Indels: 77
Gaps: 1

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US-10-791-980-6 (1-520) x US-09-950-510-11 (1-2310)

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QY      1 MetValAlaArgValGlyLeuLeuLeuArgAlaLeuGlnLeuLeuTTPGlyHisLeu 20
Db      317 ATGATGCGCGGTCTGCGCTCTGCTGGCCCTCGACAGCTCACTGTGGGGCCACTG 376
QY      21 AspAlaGlnProAlaGlyArgGlyGlyGlnLeuArgIlySGlyGlnAlaGlnAlaPheLeu 40
Db      377 GAGCGCCAGCCCGCGAGCGGAGGCGGAGGCGGAGGCTGGCAAGAGGCGGAGGCACTTCTTA 436
QY      41 GlnuTyTyrGlyTyrLeuAsnGlnGlnValProLyAsnAlaProPheSerThrArgPheSer 60
Db      437 GAGAAATACGGAATCTCTCAATGAACAGTCCCAAGACTCCACCTCCACTGATTCAAC 496
QY      61 AspAlaIleAspAlaPheGlnTTPValSerGlnLeuProValSerGlyValIleuAspArg 80
Db      497 GATGCCATCAAGGCTTCACTGAGTGTCTCCAGCTACTGTCAGCGCGTGTGACCGC 556
QY      81 AlaThrLeuArgGlnMetThrArgProArGtyrGlyValIleuAspThrAsnSerTyrAla 100
Db      557 GCCACCTGGGCGCAGATGACTGCTCCCGCTCGGGGTTACAGATACCAACAGTTATCGG 616
QY      101 AlaTTPAlaGlnArgIleSerAspLeuPheAlaArgHisArgThrIlyMetArGArglyAr 120
Db      617 GCGTGGGCTGAGAGATCACTGACTTGTGTCTTACACCGGAGCCAAATGAGGCGTGAAG 676
QY      121 IyAspArgPheAlaIlySGlnGlyAsnLyArTyrIlySGlnHisLeuSerTyrArgLeuVal 140
Db      677 AAAGCTTTGCAAG-----
QY      141 AsnTTPProGlnHisLeuArgSerArgGlnPheGlyAlaProCyAsnAlaProProSerSer 160
Db      691 -----
QY      161 CySGlyAlaThrSerGlnArgTTPSerSerGlyArgProGlnProGlnAlaProLeuThr 180
Db      691 -----
QY      181 SerGlySerProSerSerlySGlyThrThrThrMetGlyTyrPalamcProLeuMetAla 200
Db      691 -----
QY      201 Gln-GlyAlaProTTPArGThrProPheLeuProArGArglyGlyGlnAlaHisPheArgI 220

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Db	692	CAAGGGAGGCGCCCTTGAGCGACGCCCTTC - CTGCCCCCGCGGAGGACACTTCAGCA	750
Qy	220	nAspGluArGTrpSerLeuSerAArgAArgGlyAArgAanLeuPheValValLeuAlaH	240
Db	751	AGATAGGCGCTGGTCCCTGAGCGCGCGCGGCGCAACCTGTTGTGTGTGTCGCA	810
Qy	240	eGluIleGlyHThrLeuGlyLeuThrHrIAsSerProAlaProArgAlaLeuMetAlaP	260
Db	811	CGAGATCCGTCACAGCTTGGCTCAACCACTGCGCGCGCGCGCGCTCAATGGCGCC	870
Qy	260	OTyTrTyIyAArgLeuGlyAArgAAspAlaLeuLeuSerTrpAspAspValLeuAlaG	280
Db	871	CTACTACAAGAGGCTGGCGCGCGAGCGCTGCTCAGCTGGAGCAAGTCTGGCCGTGCA	930
Qy	280	nSerLeuTyArgIyAArgProLeuGlyGlySerValAlaValGlnLeuProGlyIyA	300
Db	931	GAGCTGTATGGGAAGCCCTTAGGGGGCTCAGTGGCGTCCAGCTCCAGGAAGCTGTT	990
Qy	300	eThrAspPheGluThrTrpAspSerTySerProGlnGlyAArgAArgProGluHrGln	320
Db	991	CACGTACTTGAACCTGGACTCGGACTCTCAACGCCCCCAAGAAAGCGCCCTGAACG	105
Qy	320	yProIyAArgTyCyHrIAsSerSerPheAspAlaIleThrValAspAArgGlnGlnLeuTy	340
Db	1051	CCCTAAATACTCCCACTCTTCCCTGATGCCATCACTGATAGACAGGCAACAGCACTGTA	111
Qy	340	rIlePheIyAArgIySerHrIlePheTrpGluValAlaAlaAspGlyAAspValSerGluProA	360
Db	1111	CATTTTAAAGGAGACCATTTCTGGAGAGTGCAGCTGATGGCAAGTCTCAGAGGCCCG	117
Qy	360	gProLeuGlnGluAArgTrpValGlyLeuArgProAenIleGluAlaAlaValSerIe	380
Db	1171	TCACATGCAGGAAGATGGGTGGGGTGGCCCCCAACATTAGAGCTGGCGGACTGTCA	123
Qy	380	uAsnAspGlyAAspPheTyPhePheIyAArgGlyAArgTyCySTrPArgPheAArgIyProLy	400
Db	1231	GAATGATGAGATTCTTCTACTTCTTCAAAAGGGGTGCATCTGAGAGGTTCCGGGGCCCCAA	129
Qy	400	sProValTrpGlyLeuArgProGlnLeuCyAArgAlaGlyIyLeuProAArgHsPProAspAl	420
Db	1291	GCCATGTGGGGTCTCCCAACACTGTGGCGGCGAGGGGCGCTGCCCCGCATCTAGCC	135
Qy	420	aAlaLeuPhePheProProLeuAArgArgLeuIleLeuPheIyAArgTyAArgTyA	440
Db	1351	CGCCCTCTTCTTCCCTCTCTGCGCGCTCATCTCTTCAAGGGTGGCCCGCTACAGCT	141
Qy	440	lLeuAlaArgGlyIyLeuGlnValGlnProTyTyTyProAArgSerLeuGlnAspTrpG	460
Db	1411	GCTGGCCCGAGGGGAGACTGCAGAGTGGAAGCCCTACACCCCGAAGTCTCAGAGAGCGGG	147
Qy	460	yGlyIyIleProGluGluValSerGlyAlaLeuProAArgProAspGlySerIleIlePheH	480
Db	1471	AGGCATCCCTGAGAGGTCAAGCGCGCCCTGCGGAAGCCCGATGGCTCCATCATCTTCTT	153
Qy	480	eArgAspAspArgTyTyTrpArgLeuAspGlnAlaIyAArgGlnAlaThrThSerGlyA	500
Db	1531	CCGAAATGACCGCTACCTGGCGCTCGAACAGGCCAAATGCAAGGCAACACCTCGGGCG	159
Qy	500	gTrpAlaThrGluLeuProTrpMetGlyCySTrPhAlaAsnSerGlySerAlaLeuH	520
Db	1591	CTGGGCGCACGAGCTGCCCTGGATGGGCTGTGGATGCAATCGGAGAGCGCCCTGTT	165
Qy	520 e 520		
Db	1651 c 1651		

RESULT 7
US-08-704-711A-10
; Sequence 10, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMAN, Bernd

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1  TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
2  TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
3  NUMBER OF SEQUENCES: 22
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Foley & Lardner
6  STREET: 3000 K Street, N.W., Suite 500
7  CITY: Washington
8  STATE: D.C.
9  COUNTRY: USA
10 ZIP: 20007-5109
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: PatentIn Release #1.0, Version #1.30
17
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/704,711A
20 FILING DATE: 20-NOV-1996
21 CLASSIFICATION: 435
22
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: WO PCT/DE95/00357
25 FILING DATE: 17-MAR-1995
26
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: DE 4438838.1
29 FILING DATE: 21-OCT-1994
30
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: DE 4409663.1
33 FILING DATE: 17-MAR-1994
34
35 ATTORNEY/AGENT INFORMATION:
36 NAME: GRANADOS, Patricia D.
37 REGISTRATION NUMBER: 33,683
38 REFERENCE/DOCKET NUMBER: 26083/124
39
40 TELECOMMUNICATION INFORMATION:
41 TELEPHONE: (202) 672-5300
42
43 TELEFAX: (202) 672-5399
44
45 TELEX: 904136
46
47 INFORMATION FOR SEQ. ID NO: 10:
48 SEQUENCE CHARACTERISTICS:
49 LENGTH: 3530 base pairs
50 TYPE: nucleic acid
51 STRANDEDNESS: single
52 TOPOLOGY: linear
53
54 US-08-704-711A-10
55
56 Alignment Scores:
57 Pred. No.: 5,01e-40 Length: 3530
58 Score: 602.00 Matches: 183
59 Percent Similarity: 45.12% Conservative: 71
60 Best Local Similarity: 32.50% Mismatches: 232
61 Query Match: 21.24% Indels: 78
62 DB: 3 Gaps: 20
63
64 US-10-791-980-6 (1-520) x US-08-704-711A-10 (1-3530)
65
66 Oy 9 LeuAArgAlaLeuGlnLeuLeuLeuTrpGlyHisLeuAspAlaGlnProAlaGluArgGly 28
67 Db 133 CTGCTCCCGCTGCTCTGCTGCTGCTGCGGCTGCGGCTTGGCGTGAAGC-----183
68
69 Oy 29 GlyGlnGlnLeuAArgGlySerGlnAlaGlnAlaPheLeuGluGlySerGlyTyrTrpLeuAnglu 48
70 Db 184 GCCGAAGACGCGGAGGTCCATCCGACGAGAACTGGCTGCGGCTTTAATGCTACCTGCTCAG 243
71
72 Oy 49 GlnValProIleValAlaProThrSerThrArg-----PheSerAspAlaIle 63
73 Db 244 -----CCAGCGCGCATATGTCACACATGCGCTTCCGCCCAAGATCTTGCGCTCGCCCTT 297
74
75 Oy 64 ArgAlaPheGlnTrpValSerLeuSerLeuProValSerGlyValLeuAspArgAlaThrLeu 83
76 Db 298 GCAGAGATGCAGCGCTTACCGGAGATCCACAGTCCAGTCCGCGTGTGTCGACGAAGACCAAG 357
77
78 Oy 84 ArgGlnMetThrArgProArgGlySerGlyValThrAspThrAsnSerTyrAlaAlaTrpAla 103
79 Db 358 GAGCTGATGAAGGCGCGCTGTGTGGGGTCCAGAC-----CACTTGGG 402

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QY 104 GluArg11SerAspLeuPheAlaArgHisArgThrLysMetArgArgLysIleValArgPhe 123
 Db 403 GTCAGAGTGA-----GCCAACCTGGCGGCGCTGGAGAGCGCTAC 444
 QY 124 AlaLysGlnGlyAsnLysTrpTyrLysGlnIleLeuSerTyrArgLeuValAsnTrpPro 143
 Db 445 GCCCTCAGCGGAGAGAGTGAACAACCACTGACCTTACCTTACGATCCAGAACTACACG 504
 QY 144 GluHisLeu-ArgSerArgGlnPheGlyAlaProCysAlaProProSerSerArgGlyAla 163
 Db 505 GAGAAGTTGGCTGTGTACCATCGATGAGAGCGGCTGCCAGGCGCTTCGCGTGTGGAG 564
 QY 163 aThrSerGlnArgTrpSerSerGlyArgProGlnProGlnAlaProLeuThrSerGlySe 183
 Db 565 CAGCGCAGCGCCCTGCTGTCCAGAGG-----TGCCCTATAGAGACATCCGG 612
 QY 183 rProSerSerLysGlyThrThrMetGlyTrpAlaMetPro----- 197
 Db 613 CTGCGGCGCAGAGAGAGCGGACATCATGCTACTTGGCTTGGCTTCCAGCGCGAC 672
 QY 198 -----LeuMetAlaGlnGlyAlaProTrpArgThrProPheLeuPro----- 211
 Db 673 AGCTGCGGCTTGTGTAGCAGCGGTGTCTTGTGCGCCAGCGCTAT-TTCCCTGGCCCGG 731
 QY 212 -ArgArgGlyGlnAlaHisPheAspGlnAspGlyLysTrpSerLeuSerArgArg----- 229
 Db 732 CCTAGCGGCGGACACCTTTTGTGCGCAGATGAGCGCTTGACCTTCCGACACTGACCT 791
 QY 230 -ArgGlyArgAsnLeuPheValIleuAlaHisGluIleGlyHisThrLeuGlyLeuTh 249
 Db 792 GCATGAAACAACTCTTCTGCGGAGATGAGCTGGGCGACCGCTGGGCGCTGA 851
 QY 249 rHisSerProAlaProArgAlaLeuMetAlaProTyrTyrLysArgLeuGlyArgAspAl 269
 Db 852 GCACTCCAGCAACCCCATGCACTCATGCGCGCTTACCACTGAGAGAGAGCTTGACAA 911
 QY 269 aLeu-----LeuSerTrpAspAspValIleuAlaGlnSerLeuTyrGlyLysProLeuG 288
 Db 912 CTTCAAGCTGCCGAGAGACATCTCGTGGCATCCAGCAGCTTACGGTACCCCAAGACG 971
 QY 288 Y-----GlySerValAlaValGlnLeuProGlyLys-LeuP 300
 Db 972 TCAAGCCAGACCTAACCAAGCTCTCCCACTGTGACGCCAGCGCGCGCGCGCTGA 1031
 QY 300 heThrAspPheGlnThrTrpAspSerTyrSerProGln-GlyArg----- 314
 Db 1032 CCAACGGCGCGCGCGCGCTCCCAAGCACAACCCCAAGTGGAGAGCGAGCGCGCC 1091
 QY 315 -----ArgProGlnThrGlnGlyPro 322
 Db 1092 AAAACCGGCGCGCGCGCGCTCCAGCCAGCCAGAGCGCGCGCGCATGTGCCCCAA 1151
 QY 322 eTyrCysHisSerSerPheAspAlaIleThrValAspArgGlnGlnGlnLeuTyrIleP 342
 Db 1152 CATGTGCGAGCGGAGCTTGCACAGTGGCCATGCTTGC---GGGAGATGTTCGTGT 1208
 QY 342 eLysGlySerHisPheTrpGluValAlaAlaAspGlyAsnValSerGlu--ProArgPr 361
 Db 1209 CAAGGCGCGCTGTCTGCGCAGTCCGCGCACAACCGGTCTGACACAACATCCATGCC 1268
 QY 361 oLeuGlnGlnLysArgValGlyLeuProProAsnIleGlnAlaAlaValSerLeuAs 381
 Db 1269 CATCGGCGCATCTTGGCGTGGTGTGCGCGCGGATC---AGTGTGCTCCATCAGAGCGCA 1325
 QY 381 nAspGlyAspPheTyrPhePheLysGlyArgCysTrpArgPheArgGlyProLysPr 401
 Db 1326 AGACGCTGTCTTCTTCAAGGTGACCGTATGCTCTTTCGAGAAAGCAACT 1385
 QY 401 ovalTrpGlyLeuProGln--LeuCybArgAlaGly--GlyLeuPro--ArgHisPr 418
 Db 1386 GAGACCGCGCTAACCAAGCGCGTGAACCACTATGCGCTGGGATCCCTATAGACCGCAT 1445

QY 418 oAspAlaAlaLeuPhePheProProLeuArgArgLeuIleLeuPheLysGlyAlaArgT 438
 Db 1446 TGACAGCGCATCTGTGTGGAGCCCAAGCCACACTTCTTCTTCAAGAGAGAGCTGA 1505
 QY 438 rTyrValLeuAlaArgGlyLysLeuGlnValGlnProTyrTyrProAspSerLeuGlnAs 458
 Db 1506 CTGGCGCTTCAACGAGAGACACACAGCTGAGAGACCTGGGTATCCCAAGCCCATAGTCT 1565
 QY 458 pTrpGlyGlyIleProGlnGlnValSerGlyAlaLeuProArgProAspGlySer--I 477
 Db 1566 CTGGAGGAGATCCCTGCTCCCTTAAAGGCGCTTCTGAGCAATGACGCGCTACAC 1625
 QY 477 eIlePhePheArgAspAspArgTyrTrpArgLeuAspGlnAlaLysLeuGlnAlaThrTh 497
 Db 1626 CTACTTCTTCAAGAGGACCAACAATCTGGAATTCGACAAATAGAGCGCTCGGATGAGCC 1685
 QY 497 rSerGlyArgTrpAlaThrGlnLeuLeuProTrpMetGlyCysTrp--HisAlaAsnSerG 516
 Db 1686 CGGCTAACCCCAAGTCCATCTGCGGAGCTTCATGCGCTGCCAGAGACAGCTGAGCGCAG 1745
 QY 516 Y 516
 Db 1746 C 1746

RESULT 8
 US-09-521-220-10
 ; Sequence 10, Application US/09521220
 ; Patent No. 639348
 ; GENERAL INFORMATION:
 ; APPLICANT: WILK, Horst
 ; HINZMANN, Bernd
 ; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/521,220
 ; FILING DATE: 08-Mar-2000
 ; CLASSIFICATION: <Unknown>
 ; 21-OCT-1994
 ; 17-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/704,711
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: DE 4438838.1
 ; FILING DATE: 21-OCT-1994
 ; APPLICATION NUMBER: DE 4409663.1
 ; FILING DATE: 17-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GRANADOS, Patricia D.
 ; REGISTRATION NUMBER: 33,683
 ; REFERENCE/DOCKET NUMBER: 26083/124
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 672-5300
 ; TELEFAX: (202) 672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3530 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

/ ORGANISM: Homo sapiens
US-09-171-545-7

Alignment Scores:

Pred. No.:	2,62e-38	Length:	1524
Score:	575.00	Matches:	167
Percent Similarity:	48.58%	Conservative:	72
Best Local Similarity:	33.94%	Mismatches:	184
Query Match:	20.29%	Indels:	70
		Gaps:	19

US-10-791-980-6 (1-520) x US-09-171-545-7 (1-1524)

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OY 39 PheLeuGluYerYrGlyTyLeuLeuGluGlnValProLyAlaProThrSerThrArg 58
Db 91 TACCTTCACAAATAGGTAAGCTTCAAGAGCTCTA-----GAAGATCTTAATAC 141
OY 59 Phe-----SerAlaIleArgAlaPheGlnTrpValSerGlnLeuPro 73
Db 142 TTCAGGCCAGAGATATACCGAGGCTCGAGAGCTTTTCAGAGAGCATGAACCTTCCA 201
OY 74 ValSerGlyValLeuAlaPheArgAlaThrLeuArgGlnMetThrArgProArgCySGlyVal 93
Db 202 GCTCAGGCTCAGCTGGATGATGCCACAGAGCCCGCATGAGGAGCCTCGTTGGGCTTA 261
OY 94 ThrApThrAenSerYrAlaIleAlaTrpAlaGluArgIleSerAlaPheAlaArgHis 113
Db 262 GAGGATCCCTTCAAC-----276
OY 114 ArgThrLybMetAlaGlybLybArgPheAlaIleArgGlnIleValbLybTrpLybGln 133
Db 277 -----CAGAAAGACCTTAAATACCTGTGGTGGG---CGCTGAGAAAGAAAG 321
OY 134 HisLeuSerYrAlaGlyValLeuTrpProGluHisLeu-ArgSerArgGlnPheGlyAla 153
Db 322 CACCTGACTTCGCGACTTGAACTGACCTCCACCTTCCACCCACACAGCCCGGCA 381
OY 153 aProCyAlaProProSerSerCySGlyAlaThrSerGlnArgTrpSerSerGlyAlaArgPr 173
Db 382 GCCCTGGCTCAGACCTTCCAGACTGAGCA-----ANGTGG-----CTCCC 423
OY 173 ogInProGln-----AlaProLeuThrSerGlySerProSer-----Se 186
Db 424 TTGACCTTCCAGAGAGTGACGCTGTGGCTGACATCCGCTCTCTCCATGCGCGC 483
OY 186 rLybGlyThrThrThMetGlyTrpAlaMetProLeuMetAlaGlnIleAlaProTrpAr 206
Db 484 CAAAGCTCGTACTGTT-----CCAATACTTTTGAATGGCCCTGGAGAGTCTGGCC 534
OY 206 gThrProPheLeuProArgArgGlyGluAlaHisPheAlaPheGlnAlaPheGlnArgLeu 226
Db 535 CATGCCGAC-ATCCCAAGAGCTGGGCACTGTGCACTTCACAGACAGAGTTCTGAGCTGA 593
OY 226 uSerArgAlaGlyArgAlaPheLeuPheValValLeuAlaHisGluIleGlyHisThrTr 246
Db 594 GGGGACCTAACCTGGGGTGAACCTGCGATCATTTGACAGCCATAGATGGGCCATGTCTT 653
OY 246 uGlyLeuThrHisSerProAlaProArgAlaLeuMetAlaProLyTrpLybArgLeuG 266
Db 654 GGGGCTTGGGCACTCCGATATTCACAGGCCCTCATGCCCCAGCTCAACAGGGGCTACCG 713
OY 266 YArgAlaPheAlaLeuSerTrpAlaPhePheValLeuAlaValGlnSerLeuTrpLybAr 286
Db 714 GCCCACCATTAAAGCTGACCCAGATGATGTGGCAGGAGATCTCTCATATGGCAAGAA 773
OY 286 oLeuGlyLybSerValAlaValGlnLeuProGlyLybLeuPheThrApPheGluThrTr 306
Db 774 G-----AGTCACTGATTAAGGATGAGAAAGAAAGACAGACAGCTGCCACT-- 822
OY 306 pAsPserTrSerProGlnIleArgArgProGluThrGlnGlyProLybTrCybHisSe 326
Db 823 -----GTGCCCCCACTGCCACAGAACCACTCACTCCATG---CAGACCTTGGAGTAG 872

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OY 326 rSerPheAlaIleThrValAspArgGlnGlnGlnLeuTrpIlePheLybSerHis 346
Db 873 TGAACCTGATGCCATATGCTCTGGGCCCCGGTGGAAAGCTATGCTTTCAAGGGGACTA 932
OY 346 sPheTrpGlyValAlaAlaAspGlyAsnValSerGlnProArgProLeu-----G 363
Db 933 TGTGTGACTGTATCAGATTCCAGCA-----CCGGGCCCTTGTCCAGAGTTC 980
OY 363 nGluArgTrpValGlyLeuProProAlaGlnIleAlaAlaValSerLeuAsnArg 383
Db 981 TGCCCTTTGGAGAGGGGCTCCCGGAAACCTGATGCTGTCTATCTGCTCGACACACA 1040
OY 383 YAsPheTrpPhePheLybGlyArgCybTrpArgPheArgGlyProLybProValTr 403
Db 1041 ATGATTACTCTTTAAGGAGACAGAGGTGGCGCTACATTAATTCAGATGCTCTCC 1100
OY 403 pGlyLeuProGlnLeuCybArgAlaGlyGlyLeuProArgHisPheAlaAlaLeuPh 423
Db 1101 TGGCTTCCCAAG-----AAGCTGAATAGAGTAAGAACCTTAATTCAGATGCTCTTA 1154
OY 423 ePheProProLeuArgArgLeuIleLeuPheLybGlyAlaArgTrpYr-----Va 440
Db 1155 TTGGCTCTCAACCAAGAGGTGTTCCCTTTAAGGCTCCGGTACTGGGAGTGGAGCA 1214
OY 440 lLeuAlaArgGlyGlyLeuGlnValGluProTrpYrProArgSerLeuGlnAsp---Tr 459
Db 1215 GCTAGCCGAACTGACTTCAGC-----AGCTACCCCAACCAATCAAGGTTGTT 1265
OY 459 pGlyGlyIleProGlnIleValSerGlyAlaLeuProArgProAlaPheGlySerIleAlaPh 479
Db 1266 TACGGAGTGCACAAACAGCCCTCGGCTGCTGTAAGTGGCAAGATGGCGAGTACTT 1325
OY 479 ePheArgAspAspArgTrpTrpArgLeuAspGlnAlaLybLeuGlnAlaThrThrSerG 499
Db 1326 CTTCAAGGGCAAGTCTACTGGCGCTCAACAG---CAGCTTCAGTAGAAGAAAGGCTA 1382
OY 499 YArgTrpAlaThrGluLeuProTrpMetGlyCyb 510
Db 1383 TCCCAAGAAATATTTCCCAACTGATGATGACTGT 1416

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RESULT 10

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US-09-171-545-22
/ Sequence 22, Application US/09171545
/ Patent No. 6566116
/ GENERAL INFORMATION:
/ APPLICANT: Kojima, Yoshimura
/ APPLICANT: Yuichi, Hikichi
/ APPLICANT: Atsushi, Nishimura
/ TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION AND USE
/ CURRENT APPLICATION NUMBER: US/09/171,545
/ CURRENT FILING DATE: 1999-07-26
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: Patent Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 2264
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (95)..(1618)
US-09-171-545-22

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Alignment Scores:

Pred. No.:	4.63e-38	Length:	2264
Score:	575.00	Matches:	167
Percent Similarity:	48.58%	Conservative:	72
Best Local Similarity:	33.94%	Mismatches:	184
Query Match:	20.29%	Indels:	70
		Gaps:	19

US-10-791-980-6 (1-520) x US-09-171-545-22 (1-2264)

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Qy 39 PheLeuGluValSerTyrGlyTyrLeuAsnGlnGlnValProLysAlaProThrSerThrArg 58
Db 185 TACCTGCACAAATATGGGTACCTACAGAACCTCTA-----GAAGACTCTAATAAC 235
Qy 59 Phe-----SerAspAlaIleArgAlaPheGlnTTPValSerGlnLeuPro 73
Db 236 TTCAGGCCAAGATATACCAAGAGCTGTGAGAGCTTTTCAGAGAACATCTGAACCTTCCA 295
Qy 74 ValSerGlyValIleuAspArgAlaThrLeuArgGlnMetTrpArgProArgCysGlyVal 93
Db 296 GTCTCAGGTCAAGCTGATGATGCCCAAGAGGCCCAAGAGCAAGCTCTGTGGCTTA 355
Qy 94 ThrArgThrAsnSerTyrAlaAlaTTPAlaGluArgIleSerAspLeuPheAlaArgHis 113
Db 356 GAGAGTCCCTTCAAC-----370
Qy 114 ArgThrLysMetArgArgLysLysArgPheAlaLysGlnGlyAsnLysTTPTrpLysGln 133
Db 371 -----CAGAGAACCTTAAATACCTGTGGTGGC---CGCTGAGAGAAAGAG 415
Qy 134 HisLeuSerTyrArgLeuValAsnTrpProGlnHisLeu-ArgSerArgGlnPheGlyVal 153
Db 416 CACCTGACTTTCGGATCTTGAACTGCTCCACCTTCCACCCACACAGCCCGGCA 475
Qy 153 AProCysAlaProProSerSerCysGlyValaThrSerGlnArgTrpSerSerGlyArgPr 173
Db 476 GCCCTGCTCAAGCTCCAGAGCTGAGCA-----ATGTGG-----CTCCC 517
Qy 173 GlnProLys-----AlaProLeuThrSerGlySerProSer-----Se 186
Db 518 TTGACCTTCCAGAGCTGAGCTGGTGGCTGACATCCGCTCTCTCCATGAGCCGC 577
Qy 186 TlyLeuGlyThrThrThrMetGlyTTPAlaMetProLeuMetAlaGlnGlyValaProTPAr 206
Db 578 CAAGCTGCTACTGT-----CCAATACTTTGATGGCGCCGGAAGACTTGGCC 628
Qy 206 GThrProPheLeuProArgArgGlyGlyAlaHisPheArgGlnAspGlyValTrpSerLe 226
Db 629 CATGCGGAC-ATCCAGAGCTGGGAGAGTGCATTTGCACAGAAAGAGATTCTGGAGCTGA 687
Qy 226 USerArgArgArgGlyArgAsnLeuPheValValLeuAlaHisGluIleGlyHisLeuThr 246
Db 688 GGGAGCTTACCGTGGGTGAACCTGGCATTTGCACCCATGAAGTGGGCGCAAGCTCT 747
Qy 246 UGlyLeuThrHisSerProAlaProArgAlaLeuMetAlaProTyrTyrLysArgLeuG 266
Db 748 GGGGCTTGGGACTCCGATATCCAGAGCTCTGAGCCCAAGCTCTAGAGGCTACCG 807
Qy 266 YArgAspAlaLeuLeuSerTrpAspArgValIleuAlaValGlnSerLeuTyrGlyLysPr 286
Db 808 GCCCACTTAAAGCTGACCCAGATGATGGGAGAGATCCAGGCTCTCTATGGCAAGA 867
Qy 286 OleuGlyGlySerValAlaValGlnLeuProGlyLysLeuPheThrAspPheGlnThrTr 306
Db 868 G-----AGTCCAGTATGAAGGATGAGAAAGAAAGAGAGAGAGCTGCCACAC- 916
Qy 306 PAspSerTyrSerProGlnGlyArgArgProGlyThrGlnGlyProLysTyrCysHisSe 326
Db 917 -----GTGCCCAAGTCCCAAGAACCCAGTCCCATG---CCAGACCTTGCAGATAG 966
Qy 326 TSerPheAspAlaIleThrValAspArgGlnGlnGlnLeuTyrIlePheLysGlySerHis 346
Db 967 TGAAGTGGATGCGATGATGCGGGCCCGTGGAGAAAGCTATGCTTTCAAGGGGAGACTA 1026
Qy 346 ePheTrpGluValAlaAlaAspGlyAsnValSerLysProArgProLeu-----GI 363
Db 1027 TGTGTGACTGTATGAGATTCAGAG-----CCGGGCCCTTGTCCAGAGTGC 1074
Qy 363 nGluArgTrpValGlyLeuProProAsnIleGluAlaAlaAlaValSerLeuAsnAspArg 383
Db 1075 TGCCTTTGGGAGGGGCTCCCGGAAACCTGAGATCTGTCTACTGCGCTCGAAGACCA 1134
Qy 383 YAspPheTyrPhePheLysGlyGlyArgCysTTPArgPheArgGlyProLysProValTrp 403

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Db 1135 ARGATTCACCTCTTTAAGGAGCAAGGTGTGGCTTACATTAATTCAAGATGTCTCC 1194
Qy 403 PGLyLeuProGlnLeuCysArgAlaGlyGlyLeuProArgHisProAspAlaAlaLeuPh 423
Db 1195 TGGCTTCCCAAG-----AGCTGAATAGGTATGAACCTAATCCTGATGAGCTCTCTA 1248
Qy 423 ePheProPheLeuArgArgLeuIleLeuPheLysGlyValaArgTyr-----Va 440
Db 1249 TTGGCTCTCAACCAAAAGGTCTCTTTAAGGGCTCCGGGTACTGGCAGTGGAGCA 1308
Qy 440 IleuAlaArgGlyLysLeuGlnValGluProTyrTyrProArgSerLeuGlnAsp---Tr 459
Db 1309 GCTAGCCCGAAGCTGACTTCAAC-----AGCTTACCCCAACCAATCAAGGGTTGTT 1359
Qy 459 PGLyGlyIleProGlnGluValSerGlyAlaLeuProArgProAspGlySerIleIlePh 479
Db 1360 TACGGAGTGCCAACCAAGCTCGCTGCTCTATAGTTGGCAATGGCCAGACTACTT 1419
Qy 479 ePheArgAspAspArgTyrTTPArgLeuAspGlnAlaLysLeuGlnAlaThrThrSerG 499
Db 1420 CTTCAAGGCAAAAGTCTACTGGCGCTCAACAG---CAGCTTCAAGTAAAGAAAGCTA 1476
Qy 499 YArgTTPAlaThrGluLeuProTTPMetGlyCys 510
Db 1477 TCCCAAAATATTTCCCAACACTGATGACTGT 1510

RESULT 11
US-09-171-545-23
; Sequence 23, Application US/09171545
; Patent No. 6566116
; GENERAL INFORMATION:
; APPLICANT: Koji, Yoshimura
; APPLICANT: Yuichi, Nishimura
; APPLICANT: Atsushi, Nishimura
; TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION AND USE
; FILE REFERENCE: 48712/342
; CURRENT APPLICATION NUMBER: US/09/171, 545
; CURRENT FILING DATE: 1999-07-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 2049
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (90)..(1640)
; US-09-171-545-23

Alignment Scores:
Pred. No.: 7,08e-37 Length: 2049
Score: 560.00 Matches: 173
Percent Similarity: 44.97% Conservative: 73
Best Local Similarity: 31.63% Mismatches: 194
Query Match: 19.76% Indels: 108
DB: 4 Gaps: 18

US-10-791-980-6 (1-520) x US-09-171-545-23 (1-2049)
Qy 8 LeuLeuArgAlaLeuGlnLeuLeuLeuTTPGlyHisLeuAspAlaGln-----23
Db 54 CTCAGGAGAGCTTGGAACTCTGTCTGTGGAGCACTGAGCTGGCAGCTGTGGCTG 113
Qy 24 -----ProAlaGluArgGlyGlyGlnGlnLeu-----ArgLysGluAla 36
Db 114 GCCTTCTACTTCTGTGACAGTCTCAGGCGGGCTGGGGCTTGAGAGAGAGAGCG 173
Qy 37 GluAla---PheLeuGluLysTyrGlyTyrLeuAsnGlnGlnValProLysAlaProThr 55
Db 174 GTGGATTAATCCTTGTGCAATATGGGTATCTACAGAAACCTCTCGAAGAGCT---GAT 230
Qy 56 SerThrArgPheSerAsp-----AlaIleArgAlaPheGlnTTPValSerGlnLeu 72

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231 GACTTCAGGCTGAGAAATATCAAGAGGCTCTAAGAACTTCCAGGAAGCATCTGAAGT 290
Qy 73 ProValSerGlyValLeuAspArgLalThrLeuArgGlnMetThrArgProArgCysGly 92
Db 291 CCTGTTCCGGTCATATGATGATGATCCCAAGAGGCCGCTATGAAGCAAGCCCGCTGGTGGC 350
Qy 93 ValThrAspThrAsnSerTrpAlaAlaTrpAlaGluArgLlSerAspLeuPheAlaArg 112
Db 351 CTGGAGGATCCTTTCAAC----- 368
Qy 113 HisArgThrIleMetArgArgLysLeuArgPheAlaIleGlnGlyAsnLysTrpTrpLys 132
Db 369 -----CAGAACTCTGAATAATCCTGCTTGGGCCAC--TGAAGAAAG 410
Qy 133 GlnHisLeuSerTrpArgLeuValAsnTrpProGlnHisLeuArgSerArgGlnPheGly 152
Db 411 AAGACTTGACATTCCTGATCTTGAACGTGCCCTCCACCCTCCACCTCCAGAGTCCGA 470
Qy 153 Ala-ProCysAlaIleProProSerSerCysGlyAlaIleThrSerGlnArgTrpSerSerGly 172
Db 471 GCACCTCTGCATCAAGCCTTTAAGTATTTGAGCAATGAGCCCTCCAGCTTCCGGAG 530
Qy 172 gProGlnProGlnAlaProLeuThr--SerGlySerProSerSerGlyThrThr 191
Db 531 GTGAAAGCTGGTGGGCTGATATCCCGCTCTCGTTCATGAGCCGCAAGCCCATATCTGC 590
Qy 191 rMetGlyTrpAlaMetProLeuMetAlaGlnGlyAlaProTrpArgThrProPheLeu 211
Db 591 T-----CNAACGCTTTGATGGGCTGGGAGAGCTCTGCC- CAGTCGAGAGTCC 640
Qy 211 oArgArgGlyGlyAlaHisPheAspGlnAspGluArgTrpSerLeuSerArgArgGly 231
Db 641 AGAGCTTGGAGGTACACTTGCATTAACATGATTTCTGACCGAGGCCCACTTACAGG 700
Qy 231 ValGlnLeuPheValValLeuAlaHisGlnLysLeuGlyHisThrLeuGlyLeuThrHis 251
Db 701 AGTGAACCTAACGATCATTCGCGCCCATAGAGTGGGCCACGCCCTGGGACCTTGGGCA 760
Qy 251 rProAlaProArgAlaLeuMetAlaProTrpTrpLysArgLeuGlyArgAspAlaLeu 271
Db 761 CGGATATACCCAGGACCTCATGCGCTGTTTACCTGCTGCTACCAAGCCCTTACAGGCT 820
Qy 271 uSerTrpAspAspValLeuAlaValGlnSerLeuTrpGlyLysProLeuGlyGlySer 291
Db 821 GCATCCGATGATGTGGCAGGATCCAGCGCTCATGCAAG----- 863
Qy 291 lAlaValGlnLeuProGlyLysLeuPheThrAspPheGlnThrTrpAspSerTrp 311
Db 863 ----- 863
Qy 311 oGlnGlyArgArgProGlnThrGlnGly----- 320
Db 864 -----AGAGAGCGCGAGGCCAGAAAGTAGAGAGAAAGGTGAGATGCACTGTGTC 916
Qy 321 -----ProLysTrpCysHisSerSerPheAspAla 931
Db 917 AACAGTGAACAACAAACCCAGTCCATGCCAAACCTCGACAGCATGAATGATCCAT 976
Qy 331 eThrValAspArgGlnGlnLeuTrpLlePheValGlySerHisPheTrpGluVal 351
Db 977 GATGCTAGGGGCTCGGGGAAAGACATTCCTTTAAGGTAAGTGTGCTGCTTAAC 1036
Qy 351 aAlaAspGlyAsnValSerGlnProArgProLeu-----GlnGluArgTrpVal 368
Db 1037 AGATTCAAGG-----CCAGGCGCTTGTTCGAGGTCTGCGCTTTGGAGGG 1084
Qy 368 YLeuProAsnIleGluAlaAlaAlaValSerLeuAsnAspGlyAspPheTrpPhe 388
Db 1085 GCTTCTCGAAACCTGATGCTGTCTATCTCCCGGACACAGCGGATCATTTCTT 1144
Qy 388 eLysGlyGlyArgCysTrpArgPheArgGlyProLysProValTrpGlyLeuProGln 408
Db 408 ----- 408

Db 1145 CAAGGAAACAAGGTGTGGCGGTATGTGATTTCAAGTTGTCTCGGCTTCCAGT-- 1202
Qy 408 uCysArgAlaGlyGlyLeuProArgHisProAspAlaIleuPhePheProLeuArg 428
Db 1203 -----AACTCAACAAGAGTGAACCCAACTTGAATGACGCTTCTTATGGCTGTAAATCA 1258
Qy 428 GArgLeuIleLeuPheValArgGlyAlaArgTrpTrp-----ValLeuAlaArgGly 445
Db 1259 GAAGGTGTCTTTTAAAGGCTCAGGATCTGCAATGGAGTGAATGACCAAGTCTGA 1318
Qy 445 YLeuGlnValGluProTrpTrpProArgSerLeuGlnAsp---TrpGlyLysProG 464
Db 1319 CCTAGT-----CGCTAACCCCAACCAATCAAGAACTTTCACTGAGAGTCCAGA 1369
Qy 464 uGluValSerGlyAlaLeuProArgProAspGlySerLlePhePheArgAspArg 484
Db 1370 CCAACCTCAGACACTTATGAGCTGCGCAAGATGCGCAAGTCTACTTCTTCAAGGCAAGA 1429
Qy 484 gTrpTrpArgLeuAspGlnAlaValLeuGlnAlaIleThrSerGlyArgTrpAlaThr 504
Db 1430 GTACTGGCGGCTTTAACGCAACTTTCAGTGAAGGCAAGGCTATCCAGAAATACGACACA 1489
Qy 504 uLeuProTrpMetGlyCys 510
Db 1490 C-----TGGATGCACTGT 1502

RESULT 12
US-08-704-711A-9
Sequence 9, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILK, Horst
TITLE OF INVENTION: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3437 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
us-08-704-711A-9

Alignment Scores:

Pred. No.:	3,896-36	Length:	3437
Score:	555.00	Matches:	161
Percent Similarity:	45.60%	Conservative:	67
Best Local Similarity:	32.20%	Mismatches:	220
Query Match:	19.58%	Indels:	53
		Gaps:	17

US-10-791-980-6 (1-520) x US-08-704-711A-9 (1-3437)

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Qy 37 GIUAlaPheLeuGluYerTYr-----LeuAsnGluInValPro 51
Db 219 GAAGCTTGCTACAGCAATATGCTACCTGCCGCCGGGAGACTTCAGTACCACACACAG 278
Qy 52 LysAlaProThSerThArGpHeSerApaAlaIleArgAlaPheGlnTrpValSerGln 71
Db 279 CGCTCACCCAGTCA-----CTCTCAGGGCCATCGCTGCCATGCAGAAATTTCAGGC 332
Qy 72 LeuProValSerGlyValLeuAparGalaThrLeuArgGlnMetThArgProArgCys 91
Db 333 TTGCAGATGACAGGCAAGCTGATGCAGACACCATGAAAGGCCATGAGCGCCCGATGT 392
Qy 92 GIYAlaThrAapThrAasSerTyralaIaIaTrpAlaGluArgIleSerAspLeuPheAla 111
Db 393 GGTGTTCCAGACAG-----TTTGGG 413
Qy 112 ArgHisArgThrLysMetArgArgLysArgLysArgPheAlaLysGlnGlyAsnLysTrpTy 131
Db 414 GCTGATGATCAAGGCCAATGTTGAAAGAAAGGCTACGCGATCCAGAGGTCTCAAAATGGCA 473
Qy 132 LysGlnHisLeuSerTyrrArgLeuValAsnTrp-ProGlnHisLeuArgSerArgGlnPh 151
Db 474 CATAAATGAATCATCTTCTGCATCCAGATTAACACCCCCAGGTGGCGAGATATCCACA 533
Qy 151 eGlyAlaProCysAlaProProSerSerCysGlyAlaThrSerGlnArgTrpSerSerG 171
Db 534 TACGAGGCCATTCGACAGCGCTTCGCGGTGGAGAGTGCACACACACCTGCGCTTCGCG 593
Qy 171 YArg---ProGlnProGlnAlaProLeuThrSerGlySerPro-----SerSe 186
Db 594 GAGGAGCCCTTATGCTCATCGTGAAGGCCATGAGAGCAGGCCGACATCATGATCTTC 653
Qy 186 rLysGlyThrThrThrMetGlyTrpAlaMetProLeuMetAlaGlnGlyAlaProTrpAr 206
Db 654 TTTGCCGAGGCGCTTCATGCGACGACAGCACGCCCTTCGATGAGTGAAGGCGCGCTTCGCG 713
Qy 206 gThrProPheLeuProArg-----ArgGlyGluAlaHisPheAspGlnAspGluAr 223
Db 714 CATGCTTAC-TTCCAGGCCCCCAACATTTGAGAGAGACCCACTTGTGATCTGCGAGGCC 772
Qy 223 gTrpSerLeuSerArgArg-----ArgGlyArgAsnLeuPheValaIleuAlaHisG 241
Db 773 TTGACATGTCAGAGATGAGATCTGAATGAATGACATCTTCGTGGTGCCTGACAGA 832
Qy 241 uIlleGlyHisThrLeuGlyLeuThrHisSerProAlaProArgAlaLeuMetAlaProTy 261
Db 833 GCTGGGCGCATGCTCCGCGGCTCGACATTCAGTACCCCTCGGCATCATGAGCACCTT 892
Qy 261 rTyrrLysArgLeuGly---ArgAspAlaLeuLeuSerTrpAspAspValaIleuAlaValG 280
Db 893 TTACCAAGTGAATGACACGAGAAATTTGTGCTGCGCCGATGATGACCGCGGGGACATCA 952
Qy 280 nSerLeuTyrrGlyLysProLeuGlyLysSerValaIaValGlnLeuProGlyLysLeuPh 300
Db 953 GCAACTTATATGGGGGAGTCAAGG-----TTCCCAACAAGATGCC 994
Qy 300 eThrAspPheGluThrTrpAspSerTyrrSer---ProGlnGlyArgArgProGlnThrG 319
Db 995 CCTCAACCCAGACTACTCCGCGCTTGTCTGTATAAACCAAAACCCACACTTA 1054

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Qy 319 nGlyProLysTyrrCysHisSerSerPheAspAlaIleThrValAspArgGlnGlnLe 339
Db 1055 TGGGCCCAACATCTGTACGGGAACCTTGAACCGGTGCATGCTCCGA---GGGAGAT 1111
Qy 339 uTyrrIlePheLysGlySerHisPheTrpGluVal-----AlaIleAspGlyAs 355
Db 1112 GTTGTCTTCAAGAGCGCTGTTCTGCGGGTGAAGATTAACCAAGATGATGATGA-- 1169
Qy 355 nValSerGluProArgProLeuGlnGluArgTrpValGlyLeuProProAsnIleGluAl 375
Db 1170 -----TACCAATGCCATTTGGCCACTTCTGGGGGGCTTGGCTGCTCATAC-- 1220
Qy 375 AlaAlaValSerLeuAsnAspGlyAspPheTyrrPhePheLysGlyArgCysTrpAr 395
Db 1221 -ACGCTTAAGAGAGAAAGATGGAATTCGTCTTCAAAAGAGACAGATTTGGT 1279
Qy 395 gPheArgGlyProLysProValTrpGlyLeuProGlnLeuCyArg-----AlaGlyG 413
Db 1280 GTTTGATGAGCGCTCCCTGGAACCTGCTACCCCAAGCATTTAAGAGCTGGCGGAG 1339
Qy 413 YLeuProArgHisPro---AspAlaAlaLeuPhePheProProLeuArgArgLeuIle 432
Db 1340 GCTGCTTACCGACAAAGATTAAGTGTCTCTCTTGTGATGCCAATGAGAAAGACTTACT 1399
Qy 432 uPheLysGlyAlaArgTyrrTyrrValaIleuAlaArgGlyGlyLeuGlnValGluProTy 452
Db 1400 CTTCGCTGAAACAAGTACTACCGTTTCAAGAGAGCTCAGGGGAGTGAATGAGAGTA 1459
Qy 452 rProArgSerLeuGlnAspTrpGlyGlyIleProGlnGluValSerGlyAlaLeuProAr 472
Db 1460 CCCCAAGAACATCAAAAGCTGCGAAGGAGATCTGTAGTCTCCAGAGGGTCAATTCATGG 1519
Qy 472 gProAspGlySerIle---IlePhePheArgAspAspArgTyrrTrpArgLeuAspGlnAl 491
Db 1500 CAGCATAAAGCTTCACTTACTTCTTACAGGGGAGAAATACGAAATTCACACACA 1579
Qy 491 aLysLeuGlnAlaThrThrSerGlyArgTrpAlaThrGluLeuProTrpMetGlyCys 510
Db 1580 GAAGCTGAAGGTGAAGAACGGGCTACCCCAAGTCAAGCCCTGAGGAGTGGATGGCTGC 1637

RESULT 13
US-09-521-220-9
Sequence 9, Application US/09521220
Patent No. 639348
GENERAL INFORMATION:
APPLICANT: WIL, Horst
HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
METALLOPROTEASES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/521,220
FILING DATE: 08-Mar-2000
CLASSIFICATION: <Unknown>
21-OCT-1994
17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/704,711
FILING DATE: <Unknown>
APPLICATION NUMBER: DE 4438638.1

```

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/ FILING DATE: 21-OCT-1994
/ APPLICATION NUMBER: DE 4409663.1
/ FILING DATE: 17-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: GRANADOS, Patricia D.
/ REGISTRATION NUMBER: 33,683
/ REFERENCE/DOCKET NUMBER: 26083/124
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 672-5300
/ TELEFAX: (202) 672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3437 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-521-220-9
Alignment Scores:
Pred. No.: 3,89e-36 Length: 3437
Score: 555.00 Matches: 161
Percent Similarity: 45.60% Conservative: 67
Best Local Similarity: 32.20% Mismatches: 220
Query Match: 19.58% Indels: 53
DB: 3 Gaps: 17
US-10-791-980-6 (1-520) x US-09-521-220-9 (1-3437)
QY 37 gtuatAphelengluuetyrGlyTyr-----LeuansgluInvalPro 51
Db 219 GAAGCTGTGCTACAGCAATATGGCTACCTGCCCGGGAGACCTTACCCACACACAG 278
QY 52 lvsAlaProThrSerThrArpSeserApaAlaileArGAlaPheGlnTrpValserGln 71
Db 279 CCGTCAACCCCAAGTCA-----CTCTCAGCGGCGCATCGCTGCATCAGACAGTTTAAAGCG 332
QY 72 LeuProvalSerGlyValLeuAparGAlaThrLeuAarglInMetThrArpProArgCys 91
Db 333 TTGCAGATGACAGGCAAGCTGATGACACACCATGAAAGCCCATGAGCGCCCGCATGT 392
QY 92 GlyValThrAspThrAsnSerTyxAlaAlaTrpAlaGluArgIleSerAspLeuPheAla 111
Db 393 GGTGTTCACAGACAG-----TTTGGG 413
QY 112 ArgHlsArgThrLysMetArgHlsArgLysArgPheAlaLysGlnGlyAsnLysTrpTyr 131
Db 414 GGTGAGATCAAGGCAATGTTTCGAAAGAGCGCTACGCGCATCCAGGGTCTCAAAATGGCA 473
QY 132 LysGlnHlsLeuSerTyxArgLeuValAsnTrp-ProGluHlsLeuAargSerArgGlnPh 151
Db 474 CATATGAAATACACTTTCGATCCAGAAATTAACACCCCAAGGTGGCGAGATATGCCACA 533
QY 151 eGlyAlaProCysAlaProProSerSerCysGlyAlaThrSerGlnArgTrpSerSerGln 171
Db 534 TACGAGGCGCATTCGCAAGCGCTTCGCGGTGTGGAGAGTGCACACACACCTGCGCTTCCG 593
QY 171 YArg---ProGlnProGlnAlaProLeuThrSerGlySerPro-----Serse 186
Db 594 GAGGTGCCCTTATGCCCTTACATCCGTGAGGGCCATGAGAAGCGCGCATCATCATGATCTTC 653
QY 186 rLysGlyThrThrMetGlyTrpAlaMetProLeuMetAlaGlnGlyAlaProTrpPar 206
Db 654 TTTCGCGAGGGCTTCATGCGAGACAGACCGCTTCATGATGTGAGGCGGCTTCCTGGCC 713
QY 206 gThrProPheLeuProArg-----ArgGlyGluAlaHlsPheAspGlnAspGluAr 223
Db 714 CATGCCCTAC-TTCCAGGCGCCCAACATTTGAGAGAGACACCACTTTGACTCTGCCAGCC 772
QY 223 gTrpSerLeuSerArgArg-----ArgGlyArgAsnLeuPheValAlaLeuAlaHlsGln 241
Db 773 TTGGACTGTGACGAATGAGATGTAATGAAATGATCATCTTCTGTGTGCTGTGACAGA 832
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QY 241 uLlGlyHlsThrLeuGlyLeuThrHlsSerProAlaProArgAlaLeuMetAlaProTy 261
Db 833 GTGGGCGCATGCCCTTCGGGGCTTCAGCATTCACAGTACCCCTCGGCGCATTCATGGCACCTT 892
QY 261 rTyxLysArgLeuGly---ArgApaAlaLeuLeuSerTrpAspAparAlaAlaValGln 280
Db 893 TTACAGAGTGAATGACACAGCAAGAAATTTGTCTCTGCGCATATGACCGCGGCGCATCCA 952
QY 280 nSerLeuTyxGlyLysProLeuGlyGlySerValAlaValGlnLeuProGlyLysLeuPh 300
Db 953 GCAACTTATATGGGGGTGAGTCAGGG-----TTCCCAACCAAGATGCC 994
QY 300 eThrAspPheGlnThrTrpAspSerTyxSer---ProGlnGlyArgArgProGluTrpGln 319
Db 995 CCGTCAACCCAGGACTTACCTCCGCGCTTCCTGTTCTGTATTAACCCAAACCCACCTTA 1054
QY 319 nGlyProLysTyxTyxHlsSerSerPheApaAlaileThrValAspArgGlnGlnLe 339
Db 1055 TGAGCCCAACATCTGTACGCGGAATTTGACACCGTGGCCATGCTCCGA---GGGAGAT 1111
QY 339 uTyxLlPheLysGlySerHlsPheTrpGluVal-----AlaAlaAspGlyAs 355
Db 1112 GTTGTCTTCAAGGAGCGCTGTTCTGCGGCGTGAAGAAATTAACCAAGTATGATGTA 1169
QY 355 nValSerGluProArgProLeuGlnGluArgTrpValGlyLeuProProAsnLlGluAl 375
Db 1170 -----TACCAATGCCCATTTGGCCAGTTCTGCGGGGCTCTGCTGCTCAAC-- 1220
QY 375 AlaAlaValSerLeuAsnAspGlyAspPheTyxPhePheLysGlyGlyArgCysTrpPar 395
Db 1221 -ACTGCTTACAGAGAGAGAGATGGCAAAATTCGTTCTTCAAGAGACAGCATTTGGGT 1279
QY 395 gPheArgGlyProLysProValTrpGlyLeuProGlnLeuCysArg-----AlaGlyGln 413
Db 1280 GTTGTATGAGGCGTCCCTGGAACCTGCACTCCCAAGCAATTAAGAGCTGGCGCAAG 1339
QY 413 YLeuProArgHlsPro---AspAlaAlaLeuPhePheProProLeuAspArgLeuLle 432
Db 1340 GTCGCTACCGCAACAAATGATGATCTCTCTCTTCTGATGCCAATGAAAGACCTACTT 1399
QY 432 uPheLysGlyAlaAspTyxTyxValLeuAlaArgGlyGlyLeuGlnValGluProTyx 452
Db 1400 CTTCCGTGAAACAACTACTACCGTTTCAACAGAAAGCTCAGGGGAGTGGATAGCGAGTA 1459
QY 452 rProAspSerLeuGlnAspTrpGlyGlyLlProGluGluValSerGlyAlaLeuProAr 472
Db 1460 CCCCAGAAACATCAAGTCTTGGAAAGGATCCCTGAGTCTCCAGAGGGTCAATTCATGGG 1519
QY 472 gProAspGlySerIle---LlPhePheAspAspAspArgTyxTrpArgLeuAspGlnAl 491
Db 1520 CAGCGATGAAGTCTTCACTTACTTCTTCAAGGGGAAACAAATCTGAAATTCACACACA 1579
QY 491 AlLysLeuGlnAlaThrThrSerGlyArgTrpAlaThrGluLeuProTyxMetGlyCys 510
Db 1580 GAAGCTGAAGTGAACCGGGCTTACCCAGTCAAGCTCTGAGGAGCTGATGGGCTGC 1637
RESULT 14
US-09-919-497-34
/ Sequence 34, Application US/09919497
/ Patent No. 6773883
/ GENERAL INFORMATION:
/ APPLICANT: Muller, George L.
/ TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
/ FILE REFERENCE: B0801/7225
/ CURRENT APPLICATION NUMBER: US/09/919,497
/ PRIOR FILING DATE: 2001-07-31
/ PRIOR APPLICATION NUMBER: US 60/221,735
/ NUMBER OF SEQ ID NOS: 100
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 34
/ LENGTH: 3437
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TYPE: DNA
ORGANISM: Homo sapiens
US-09-919-497-34

Alignment Scores:

Pred. No.:	3,896-36	Length:	3437
Score:	555.00	Matches:	161
Percent Similarity:	45.60%	Conservative:	67
Best Local Similarity:	32.20%	Mismatches:	220
Query Match:	19.58%	Indels:	53
DB:	4	Gaps:	17

US-10-791-980-6 (1-520) x US-09-919-497-34 (1-3437)

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OY 37 GUAAlaPheLeuGluYerGlyTYr-----LeuAenGluGlnValPro 51
DB 219 GAAGCTGGCTACACATATGGCTACCTGCTCCCGGGAGCTACGATCCACACACAG 278
OY 52 LybAlaProThrSerThrArgPheSerApaAlaIleArgAlaPheGlnTrpValSerGln 71
DB 279 CGCTCACCCAGTCA-----CTCTCAGCGGCATCGCTGCATGACAGAAATTTCAGGC 332
OY 72 LeuProValSerGlyValLeuAparGalaThrLeuArgGlnMetThrArgProArgCys 91
DB 333 TTGCAAGTAACAGGAAAGCTGTACAGACACACATGAGCCATGAGGCGCCCGCATGT 392
OY 92 GlyValThrAerPThrAerSerTyraIaIaIaTrpAlaGluArgIleSerAerPheAla 111
DB 393 GGTGTTCCAGACAG-----TTTGGG 413
OY 112 ArgAlaArgThrLyMetArgArgLybValArgPheAlaLybGlnGlyAenLybTrpTy 131
DB 414 GCTGATACAGAGCCCAATGTTGAGAAAGCGCTACGCGCATCAGAGGTCAATGCGAA 473
OY 132 LybGlnAlaSerSerTyraArgLeuValAenTrp-ProGlnIleLeuAerSerArgGlnPh 151
DB 474 CATAAATGAATCATCTTCTGATCCAGAAATTAACCCCCCAAGGTGGCGGAGTATGCCA 533
OY 151 eGlyAlaProCysAlaProProSerSerCysGlyAlaThrSerGlnArgTrpSerSerG 171
DB 534 TACGAGGCTATTCGACAGCGCTTCGCGGTGGAGAGTCCACACACACATGCGCTTCCG 593
OY 171 YArg--ProGlnProGlnAlaProLeuThrSerGlySerPro-----SerSe 186
DB 594 GAGGTGCGCTTATGCTTACATCCGTGAGGCGCATGAGAGCAGCGGCATCATGATCTTC 653
OY 186 rLybGlyThrThrMetGlyTrpAlaMetProLeuMetAlaGlnGlyAlaProTrpArg 206
DB 654 TTTGCCGAGGCTTCATGCGACAGCAGCGCTTCGATGTGAGGCGGCTTCCGTGGCC 713
OY 206 GThrProPheLeuProArg-----ArgGlyGlnAlaIleAerPheGlnAerGlnAla 223
DB 714 CATGCTTAC-TTCCAGGCGCCCAACATTTGAGAGAGACCCCTTGTGACTTGGCGAGCC 772
OY 223 gTrpSerLeuSerArgArg-----ArgGlyArgAlaIleAerPheGlnAerGlnAla 241
DB 773 TTGAGCTGACAGAAATGAGATGTGAATGAAATGACATCTTCGTGGTGGCTGTGACGA 832
OY 241 uIlleGlyHilbTrLeuGlyLeuThrHilbSerProAlaProAlaAlaLeuMetAlaProTy 261
DB 833 GCTGGGCGCATGCGCTCGGGCTCGAGCATTCACAGTCCCTTCGATCATGAGCACTT 892
OY 261 rTyTrpAerGlyLeuGly---ArgApaAlaLeuLeuSerTrpAerApaValLeuAlaValG 280
DB 893 TTACCAAGTGAATGACACGAGAAATTTTGTCTGCCCATGATGACCGCGGGGATCCA 952
OY 280 nSerLeuTyraLybProLeuGlyLybSerValAlaValGlnLeuProGlyLybLeuAerPh 300
DB 953 GCACCTTATGAGGGGAGTCAAGG-----TTCCCCACCAAGATGCC 994
OY 300 eThrAerPheGlnTrpAerSerTyra---ProGlnGlyArgArgProGlnTrpG 319
DB 995 CCTCAACCCAGAGACTACCTCCGGCGTTCTGTCTGTATAAACCCAAACCCACCTTA 1054

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OY 319 nGlyProLybTyraCysHilbSerSerPheApaAlaIleThrValAerArgGlnGlnLe 339
DB 1055 TGGGCCCAACATCTGTACGGGAACTTTGACACCGGTGCATGTCCGA---GGGAGAT 1111
OY 339 uTyTrlPheLeuGlySerHilbPheTrpGluVal-----AlaAlaAerGlyAs 355
DB 1112 GTTGTCTTCAAGAGCGCTGTGCGGGGTGAGAAATTAACCAAGTATGATGAGA-- 1169
OY 355 nValSerGluProArgProLeuGlnGlnAlaTrpValGlyLeuProProAenIleGlnAl 375
DB 1170 -----TACCAATGCCCATTTGGCCAGTTCGGGGGGCTTGGCTGCTCATAC-- 1220
OY 375 aAlaAlaValSerLeuAenAerGlyAerPheTyraPheLeuGlyGlyArgCysTrpArg 395
DB 1221 -ACTGCTTACAGAGAGAAAGATGGAAATTTGCTTCTTCAAGAGACAGCATTTGGGT 1279
OY 395 gPheArgGlyProLybProValTrpGlyLeuProGlnLeuCybArg-----AlaGlyG 413
DB 1280 GTTTGATGAGCGCTCCCTGGAACCTGCTACCCCAAGACATTAAGAGCTGGCGCGAGG 1339
OY 413 YLeuProArgHilbPro---AerAlaAlaLeuPhePheProProLeuAerArgLeuIleLe 432
DB 1340 GCTGCTTACCAAGATTTGATGCTGCTCTTCTTGATGCGCCATGAGAAACCTACTT 1399
OY 432 uPheLybGlyAlaArgTyraTyraValLeuAlaArgGlyLybLeuGlnValGluProTy 452
DB 1400 CTTCCGTGAAACAAAGTACTACCGTTTCAAGAGAGCTCAGGCGGAGTATGAGAGTA 1459
OY 452 rProArgSerLeuGlnAerTrpGlyLybIleProGlnGluValSerGlyAlaLeuProAr 472
DB 1460 CCCCAGAAACATCAAAAGTCTGGAGAGGATCCCTGAGTCTCCAGAGGTCTCATTCATGG 1519
OY 472 gProAerGlySerIle---IlePhePheArgAerAparGlyTrpArgLeuAerGlnAl 491
DB 1520 CAGCATGAAGCTTCACTTACTTCTTACAGAGGAAACAAATCTGAAATTCACACACA 1579
OY 491 aLybLeuGlnAlaThrThrSerGlyArgTrpAlaThrGluLeuProTrpMetGlyCys 510
DB 1580 GAAGCTGAAGTAAGTAAGCGGCTACCCCAAGTACAGCCCTGAGGAGCTGATGGCTGC 1637

RESULT 15
US-08-448-489-2
; Sequence 2, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-448-489-2

Alignment Scores:
Pred. No.: 4,646-36 Length: 3403
Score: 554.00 Matches: 161
Percent Similarity: 45.60% Conservative: 67
Best Local Similarity: 32.20% Mismatches: 220
Query Match: 19.55% Indels: 53
DB: 3 Gaps: 17

US-10-791-980-6 (1-520) x US-08-448-489-2 (1-3403)
OY 37 GUAAlaPheLeuGluYerGlyTYr-----LeuAenGluGlnValPro 51

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Db      217 GAAGCTGGCTACGCAATATGGCTACCTCCCGGGACCTACGTACCCAGCAACAG 276
Qy      52 LysAlaProThrSerThraRphSerAraIaiIeArgAlaPheGlnTrpValSerGln 71
Db      277 CCTCACCCCAAGTCA-----CTCTCAGCGGCCATCGCTCCACAGCAAGATTTTACGGC 330
Qy      72 LeuProValSerGlyValLeuAparArgAlaThrLeuAargGlnMetThrArgProArgCys 91
Db      331 TTGCAGATACACAGGCAAGAGCTGATGACAGACCATGAAAGGCGCATGAGCGCCCGCATGT 390
Qy      92 GlyValThrAspThrAsnSerTyrAlaIaIaIaIaIaGluValGlieSerAparLeuPheAla 111
Db      391 GGTGTTCCAGACAAAG-----TTTGGG 411
Qy      112 ArgHisArgThrLysMetCysArgLysLysArgPheAlaLysGlnGlyValAsnLysTrpTyr 131
Db      412 GCTGAGATCAAGGCCCATGTTCTGAAGAGCGCTTACGCCATCCAGGCTCTCAATGGCAA 471
Qy      132 LysGlnHisLeuSerTyrArgLeuValAsnTrp-ProGlnHisLeuArgSerArgGlnPhe 151
Db      472 CATATGAATTAATTAATTTCTGTGCATCCAGAAATTAACCCCAAGGTGGCGAGTATGCCACA 531
Qy      151 eGlyAlaProCysAlaProProSerSerCysGlyAlaIaIaThrSerGlnAargTrpSerSerG 171
Db      532 TACGAGGCCATTCCGCAAGCGCTTCCGGGTGGAGAGTCCACACCACTGCGCTTCCGC 591
Qy      171 YArg---ProGlnProGlnAlaProLeuThrSerGlySerPro-----SerSe 186
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Qy      186 rLysGlyThrThrMetGlyTrpAlaMetProLeuMetAlaGlnGlyAlaProTrpArg 206
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Qy      206 gThrProPheLeuProArg-----ArgGlyGlnAlaHisPheAspGlnAspGluArg 223
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Qy      223 gTrpSerLeuSerArgArg-----ArgGlyArgAsnLeuPheValValLeuAlaHisG 241
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Qy      280 nSerLeuTyrGlyLysProLeuGlyGlySerValAlaValGlnLeuProGlyLysLeuPhe 300
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Qy      339 uTyrIlePheLysGlySerHisPheTrpGluVal-----AlaAlaAspGlyAs 355
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Qy      355 nValSerGluProArgProLeuGlnGluArgTrpValGlyLeuProProAsnIleGluAl 375
Db      1168 -----TACCAATGCCCATTTGGCCAGATTCTGGCGGGCTGCTGCGCTCATCAAC-- 1218
Qy      375 aAlaAlaValSerLeuAsnAspGlyAparPheTyrPhePheLysGlyGlyArgCysTrpArg 395
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Qy      413 yLeuProAparHisPro---AparAlaIaLeuPhePheProProLeuAparArgLeuIleLe 432
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Qy      432 uPheLysGlyAlaArgTyrTyrValLeuAlaArgGlyLysLeuGlnValGluProTyrTyr 452
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 Job time : 303 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2005, 05:24:43 ; Search time 6714 Seconds

(without alignments)
3752.862 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2834	100.0	1597	6	AR534532 Sequence
2	2834	100.0	1597	6	AX358477 Sequence
3	2792	98.5	1560	6	AX398367 Sequence
4	2792	98.5	1563	6	AX206683 Sequence

5	2792	98.5	1817	9	AF219624 Homo sapi
6	2792	98.5	1985	6	AR528524 Sequence
7	2792	98.5	1985	6	AX464010 Sequence
8	2792	98.5	1985	6	AY358987 Homo sapi
9	2792	98.5	2241	6	AX083147 Sequence
10	2792	98.5	2484	9	AF330002 Homo sapi
11	2792	98.5	2527	6	AX398365 Sequence
12	2784	98.2	1753	9	AF315683 Homo sapi
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ALIGNMENTS

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DEFINITION Sequence 3 from patent US 6734005.
ACCESSION AR534532
VERSION AR534532.1 GI:53924838
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1597)
AUTHORS Wood T., Ekblom J., Holmgren E. and Kihlen M.
TITLE Matrix metalloproteinases
JOURNAL Patent: US 6734005-A 3 11-MAY-2004;
FEATURES
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ORIGIN

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Score: 2834.00 Length: 1597
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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QY	41	GlnArgTrpGlyTrpLeuAaGlnGlnValProLysAlaProPheSerThrArgPheSer	60
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QY	61	AspAlaIleArgAlaPheGlnTrpLysSerGlnLeuProValSerGlyValLeuAspArg	80
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QY	141	AsnTrpProGlnHisLeuArgSerArgGlnPheGlyValaProCysAlaProProSerSer	160
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QY	441	LeuAlaArGlyGlyLeuGInValGluProTYrTYrProArGSerLeuGInAspTrpGly	460
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QY	481	ArgAspAspArgTYrTrPArGLeuAspGInAlaIlyLeuGInAlaTrhTrhSerGlyArG	500
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DEFINITION	Sequence 3 from Patent WO0190326.					
ACCESSION	AX358477					

KEYWORDS

SOURCE	Homo sapiens (human)
ORGANISM	Human

STATISTICS

REFERENCE

1. Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

AUTHORS

NOVEL matrix metalloproteinases
Patent: WO 0190326-A 3 29-NOV-2001;
PHARMACIA & UPJOHN COMPANY (US)

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ORIGIN

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Alignment Scores:

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 LOCUS AX398367
 DEFINITION Sequence 3 from Patent WO0220739.
 ACCESSION AX398367
 VERSION AX398367.1 GI:21261134
 KEYWORDS
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 ORGANISM
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 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
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 CURTIS, R.A.
 TITLE Human matrix metalloproteinase
 JOURNAL Patent: WO 0220739-A 3 14-MAR-2002;
 Millennium Pharmaceuticals, Inc. (US)
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AUTHORS Lohi,J., Wilson,C.L., Roby,J.D. and Parks,W.C.
TITLE EpiLysin, a novel human matrix metalloproteinase (MMP-28) expressed in testis and keratinocytes and in response to injury
JOURNAL J. Biol. Chem. 276 (13), 10134-10144 (2001)
MEDLINE 21167821
PUBMED 11121398
REFERENCE 2 (bases 1 to 1817)
AUTHORS Lohi,J.L., Wilson,C.L., Roby,J.D. and Parks,W.C.
TITLE Direct Submission
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Db GCTGCGCGGAGGAGGACTGCAAGTGAAGCCCTTACCTACCCCGAAGTGTGCGAGG 1584
QY 460 YGlyIleProGlnuYerValSerGlyAlaLeuProArgProAspGlySerIleIlePhePh 480
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QY 480 eArgAspAspArgTyTrpArgLeuAspGlnAlaLeuGlnAlaThrThrSerGlyAr 500
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QY 500 GTrpAlaThrGlnuYerProTrpMetGlyCysTrpHisAlaAsnSerGlySerAlaLeuPh 520
Db CTGGGCGCACCGAGCTGGCTGTGATGGGCTGCTGCGATGCCAACTCGGGGAGCGCTG 1764
QY 520 e 520
Db 1765 C 1765

RESULT 7
AX464010 1985 bp DNA Linear PAT 16-JUN-2002
LOCUS
DEFINITION Sequence 143 from Patent WO0140466.
ACCESSION AX464010
VERSION AX464010.1 GI:21899022
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Baker,K.P., Bersini,M., Deforge,L., Desnoyers,L., Flivieroff,B.,
Go,W.O., Gerlensen,M.E., Goddard,A., Goddard,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tumes,D., Metanabe,C.K.,
Wood,W.L. and Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
same
Patent: WO 0140466-A 143 07-JUN-2001;
JOURNAL Genentech Inc. (US)
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source location/Qualifiers
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Db 1594 C 1594

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LOCUS AF330002 2484 bp mRNA linear PRI 07-FEB-2001

DEFINITION Homo sapiens matrix metalloprotease MMP25 mRNA, complete cds.

ACCESSION AF330002

VERSION AF330002.1 GI:12698851

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 2484)

Southan,C. and Hughes,S.A.

Cloning and genomic localization of a novel matrix metalloprotease

TITLE

Unpublished

2 (bases 1 to 2484)

Southan,C. and Hughes,S.A.

Direct Submission

Submitted (19-DEC-2000) Bioinformatics Target Discovery, SmithKline Beecham Pharmaceuticals, Third Avenue, Harlow, Essex CM3 5AW, UK

FEATURES

Source

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Location/Qualifiers

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LAOSLYKRPFGGSVAVALPKLFTDFETDNTSYSPQGRFETQPKYCHSFDATYD
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ORIGIN

Alignment Scores:

Prod. No.: 1.87e-111 Length: 2484

Score: 2792.00 Matches: 519

Percent Similarity: 99.62% Conservative: 0

Best Local Similarity: 99.62% Mismatches: 1

Query Match: 98.52% Indels: 2

DB: 9 Gaps: 0

US-10-791-980-6 (1-520) x AF330002 (1-2484)

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Qy 21 AaphlaGlnProAlaGluArgGlyGlyGlnGluLeuArgGluAlaGluAlaIleu 40

Db 336 GAGCCGCCAGCCCGCGAGCGCGAGGCCAGAGCTGCCCAAGAGAGCGGAGCAATTCCTA 395

Qy 41 GluIleuArgGlyTyrLeuAlaGlnGluAlaProIleuValaProThrSerThrArgPheSer 60

Db 396 GAGAAATACGATACCTCAATGAACAGGCTCCCAAGCTCCACCTCCACTGCAATTCAGC 455

Qy 61 AaphlaIleArgAlaPheGlnTrrValSerGlnLeuProValSerGlyValIleuAspArg 80

Db 456 GATGCATCAAGAGCGTTTCAGTGGGTGTCCAGCTACCTGTCAGCGGCGTGTGACCGC 515

Qy 81 AlaThrLeuArgGlnMetThrArgProArgGlyValThrAspThrAsnSerTyrAla 100

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Db 576 GCTCGGGCTGAGAGATCAATGACTTGTCTCTAGACCCGAGACCAAAATAGAGGGGTAAAG 635

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Db 1055 CTACTACAAAGAGGCTGGGCGCGCGCTGCTGAGTGGAGACGAGCTGGCGCGTGA 1114

Qy 280 nSerIleuTrrpIlypProLeuGlnGlyIleValAlaValGlnLeuProGlyIlypLeuPhe 300

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Db 1355 TCACCTGCAAGAAAGATGGTGGCGCTGCCCGCCCAACTTAAGGCTGGCGAGTGTCTT 1414

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Db 1535 CGCCCTCTTCTTCCCTCTCTGCGCGCTCATCTCTTCAAGAGGTGCCCTACTACGT 1594

Qy 440 lleuAlaArgGlyGlyLeuGlnValGluProTrrpTrrpProArgSerIleuGlnAspTrrpG 460

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 Db 1655 AAGCATCCCTGAGAGAGCTCAGCGGCGCTCCGAGGCGCCGATGGCTCATATCTTT 1714
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 Qy 500 GTTAlaThrGluLeuProTTPMetGlyCysTTPHISAlaIleSerGlySerAlaLeuPh 520
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 Qy 520 e 520
 Db 1835 C 1835

RESULT 11
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 LOCUS AX398365
 DEFINITION Sequence 1 from Patent WO0220739.
 ACCSSION AX398365
 VERSION AX398365.1 GI:21261133
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Human matrix metalloproteinase
 TITLE Patent: WO 0220739-A 1 14-MAR-2002;
 JOURNAL Millennium Pharmaceuticals, Inc. (US)
 FEATURES
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 /organism="Homo sapiens"
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ORIGIN

Alignment Scores:
 Pred. No.: 1.9e-111 Length: 2527
 Score: 2792.00 Matches: 519
 Percent Similarity: 99.62% Conservative: 0
 Best Local Similarity: 99.62% Mismatch: 1
 Query Match: 98.52% Indels: 2
 Gaps: 0

US-10-791-980-6 (1-520) x AX398365 (1-2527)

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 Db 360 GAGGCCAGCCCGCGAGCGCGGAGGCGAGAGCTGCGAAGAGGCGGAGGCAATTCCTA 419
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 Db 480 GATGCGCATCAGAGCGTTCAGTGGGTGTCCAGACTACCTGTCAAGCGGCTTGGACCGC 539
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RESULT 12
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LOCUS Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete
DEFINITION
ACCESSION AFJ15683
VERSION AFJ15683.1 GI:11935131
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1753)
AUTHORS Marchenko,G.N. and Strongin,A.Y.
TITLE MMP-28, a new human matrix metalloproteinase with an unusual
cysteine-switch sequence is widely expressed in tumors
JOURNAL Gene 265 (1-2), 87-93 (2001)
MEDLINE 21153427
PUBMED 11255011
REFERENCE 2 (bases 1 to 1753)
AUTHORS Marchenko,G.N. and Strongin,A.Y.
TITLE Direct Submision
JOURNAL Submitted (23-OCT-2000) The Burnham Institute, 10901, North Torrey
Planes Road, CA 92037, USA

FEATURES
source location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 2,956-111 Length: 1753
Score: 2784.00 Matches: 518
Percent Similarity: 99.42% Conservative: 0
Best Local Similarity: 99.42% Mismatches: 2
Query Match: 98.24% Indels: 2
DB: 9 Gaps: 0

US-10-791-980-6 (1-520) x AFJ15683 (1-1753)
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Db 16 ATGGTCGGGCGCGCGGCTCTCTCTGCGCCCTCGACGCTGCTACTGTGTGGGCGCACTTG 75
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RESULT 13
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 LOCUS BC002631 2091 bp mRNA linear PRI 29-JUN-2004
 DEFINITION Homo sapiens matrix metalloproteinase 28, transcript variant 2,
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 VERSION BC002631.2
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Rodrigues, S.,
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 Butlerfield, Y.S., Krzyzinski, M.I., Skalski, U., Smalins, D.E.,
 Scherlock, A., Schein, J.E., Jones, S.J., and Marra, M.A.,
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932

REFERENCE

2 (bases 1 to 2091)
 Strausberg, R.
 Direct Submission
 Submitted (05-FEB-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 On Aug 19, 2003 this sequence version replaced gi:12803592.
 Contact: MGC help desk
 Email: cgabs-help@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Sequencing Center (NISC), National Institutes of Health Intramural
 Gaithersburg, Maryland
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
 Ahter, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
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REMARK

FEATURES

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gene

CDS

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 ORGANISM Unknown.
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 AUTHORS Falduto,M.T., Magnuson,S.R. and Morgan,D.W.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OW protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2005, 07:21:52 ; Search time 4896 Seconds
(without alignments)
4042.774 Million cell updates/sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_eest2:*
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6: gb_eest5:*
7: gb_eest6:*
8: gb_g981:*
9: gb_g982:*

Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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7	1089	38.4	1086	4	BMS44516 AGENCOURT
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	13	869	30.7	499	5	BX280995	BX280995
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CR590246
LOCUS
DEFINITION full-length cDNA clone CSD1075Y06 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR590246
VERSION CR590246.1 GI:50471053
KEYWORDS HTC; CNS17_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1. (bases 1 to 1658)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1658)
REFERENCE
1. (bases 1 to 1658)
Genoscope.
Direct Submission
Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail: sequef@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. 1658
/organism="Homo sapiens"

COMMENT
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. 1658
/organism="Homo sapiens"

Yoneeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kito, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

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QY      300  ethrAapphegiuTrnTrpAasertySerProGlnGlyAArgArProGluThrGlnG 320
Db      1066  CACTGACTTGTGAGGCTGTGGAGACCCCAACACTCCAGACAGACAGCCCGGAAACAGAGG 1125
QY      320  yProLyTyTCyehHsserSerPheAapAlaIleTrValaPArgGlnGlnLeuTy 340
Db      1126  TCCTAAATACCTGCACTTCTTGTGATGTCATCACTGTA----- 1165
QY      340  rIleheltyeGlySerHisPheTrpGluValAlaAlaAapGlyAenValSerGluProAr 360
Db      1166  -----GAGCTCG 1173
QY      360  gProLeuGlnGlyAArgTrpValGlyLeuProProAanIleGluAlaAlaValaIleSer 380
Db      1174  TCCACTACAGAAAGATGGCCAGAGACTGCACCTGTGATGAGCTCTCCAGAGTCTT 1233
QY      380  uAanAapGlyAapPheTyTrpPhePheGlyGlyAArgCyETrPArgPheAArgGlyProLy 400
Db      1234  GGAAGATGAGACTTCTACTTCTTAAAGGGAATCGTGTGAGAGGTTCCAGGGCAGCA 1293
QY      400  sProValITrpGlyLeuProGlnLeuCyAArgAlaGlyGlyLeuProArgHisProAapAl 420
Db      1294  GTCCGTGTGGGGGTTCGACAGCTCTCCGCGAGGTGTACCCCGACCCGAGCG 1353
QY      420  aAlaLeuPhePheProProLeuAArgArgLeuIleLeuPheLyGlyAlaAArgTyTyVa 440
Db      1354  AGCTCTCTTCTTCCCGCTCTGCGCGCCCTAGTCCCTTCAAGGGTTCCCTCTACTAGT 1413
QY      440  lLeuAlaAArgGlyGlyLeuGlnValaGlnProTyTyTyTyProAArgSerLeuGlnAapTrpG 460
Db      1414  GCTAGCTCAAGAGAGGAGTCAAGTGGAGCCCTACTATCCCGCAGCTCGCAGACTGGCG 1473
QY      460  yGlylLePProGlnGlnValaSerGlyAlaLeuProAArgProAapLySerIleIlePhePh 480
Db      1474  CGGTGTCCCGGAGAGAGTCAAGCGCGCTCGCAAGGCGGATGCTCCATATCTTCT 1533
QY      480  eArgAapAapAArgTyTyTrpAArgLeuAArgGlnAlaIleValaIleThrThrSerGlyAr 500
Db      1534  CAGAGATGACCACTATTGGCATTTGGATCAAGCCAACTGGGGTGTACCAAGCTCCGGT 1593
QY      500  gTrpAlaThrGlnLeuLeuProTrpMetGlyCyETrPArgAlaAanSerGlySerAlaLeuPh 520
Db      1594  CTGGGCTACCGAGCTGTCTGATGGGCTGTGGATGGCACTCAAGAGGTGCCCTGTT 1653
QY      520  e 520
Db      1654  C 1654

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http://image.llnl.gov
 Plate: LLM11626 row: 0 column: 04
 High quality sequence stop: 821.
 Location/Qualifiers
 1. 822
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5248347"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb. Insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC Library."

Alignment Scores:
 Pred. No.: 2,548-100
 Score: 1420.00
 Percent Similarity: 97.458
 Best Local Similarity: 97.458
 Query Match: 50.118
 DB: 4
 Gaps: 0

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QY      119  ArgLyTyAArgPheAlaValaGlnGlyAanLyETrPTrpTyGlnHisLeuSerTyTrArg 138
Db      2  CCTAAGAAACCGTTTGCAAGACAGGTACAAATGTGTACAGAGACCTTCTCTACCGC 61
QY      139  LeuValaEntPpProGlnHisLeu-ArgSerAArgGlnPheGlyAlaProCyAlaAProPr 158
Db      62  CTGGTGAACCTGGCTGTGAGCATGTGCGGAGCCGCGCATTTGGGGGCGCGTGGCGGCC 121
QY      158  oSerSerCyGlyAlaAThrSerGlnAArgTrpSerSerGlyAArgProGlnProGlnAlaPr 178
Db      122  TTCCAGTTGTGGAGCAACCTTCAAGGCTGAGGAGTCTGGAGAGCCCGCAGCCAGCGCC 181
QY      178  oLeuThrSerGlySerProSerSerTyGlyThrThrThrMetGlyTrpAlaMetProLe 198
Db      182  GCTGACATCCGGCTCACTTCTTCCAGAGGAGCCACAAAGATGGAGTGGCAATGCTCTT 241
QY      198  uMetAlaGlnGlyAlaProTrpAArgTrpProPheLeuProAArgGlyGlyAlaHisPh 218
Db      242  GATGGCCCAAGGGGGGCGCTGCGCCAGCTTC-CTGCCCGCGCGGGAAGCGGACATT 300
QY      218  eAapGlnAapGlnAArgTrpSerLeuSerAArgAArgGlyAArgAanLeuPheVala 238
Db      301  CGACCAAGATGAGCGCTGTGTCCTGAGCCGCCCGCGGCGCCACACTGTGTGTGTCT 360
QY      238  uAlaHisGlnGlyAlaHisThrLeuGlyLeuThrHisSerProAlaProAArgAlaMet 258
Db      361  GCGCGAGAGATGGGTCAACAGCTTCAACCACTACCCGCGCGCGCGGCTCAT 420
QY      258  tAlaProTyTyTyAArgLeuGlyAArgAapAlaLeuLeuSerTrpAapAapVala 278
Db      421  GCGCGCTTACTTACAAAGAGCTGGGCGGAGCGCGTGTGCTGAGTGGAGCAAGTGTGGC 480
QY      278  aValGlnSerLeuTyTyTyAArgLeuGlyAArgProLeuGlyAArgValaAlaGlnLeuProGly 298
Db      481  CTTGCAAGCTCTGTATGGGAAGCCCTTACGGGCTCATGAGCGGTCCAGCTCCAGGAA 540
QY      298  sLeuPheThrAapPhegiuTrnTrpAasertyTySerProGlnGlyAArgArProGlnTh 318
Db      541  GCTGTTCAGTCTTGTGAGACTGGAGCTCTTACAGCCCGCAAGAGAGCGCTGAAAC 600

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RESULT 3
 B1914743
 LOCUS
 DEFINITION 822 bp mRNA linear EST 17-OCT-2001
 603184116F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5248347 5',
 mRNA sequence.
 B1914743
 VERSION
 B1914743.1 GI:16199027
 EST.
 KEYWORDS
 Homo sapiens (human)
 SOURCE
 Homo sapiens
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 822)
 NIH-MGC http://mgs.nci.nih.gov/
 AUTHORS
 National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 Unpublished (1999)
 JOURNAL
 Contact: Robert Strauberg, Ph.D.
 COMMENT
 Email: cgabre-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

Qy 318 tGInGlyProLyvTyCyvHIsSerSerPheAaPaLaIeThVaIaSPaRGInGInG 338
Db 601 GCAGGCCCCCTTAATACGGCACTTCCTTCGATGCGATCAGTGA CAGGCAACAGCA 660
Qy 338 nLeuTyTlIePheLyvGlySerThIaPheTrpGlyVaIaIaAaSPaRGlyVaSPaRG 358
Db 661 ACTGTAACATTTTACAGGAGGACCTTCGAGAGGTGAGCTGAAGCGACGTCACAA 720
Qy 358 u-PrArPProLeuGInGlyAaRGTrpVaIGlyLeuProProAaInIeGlyAaIaAa 378
Db 721 AGCCCGTCATCGACGAGAAAGATGAGTGGGCTGCCCAACATTGAGGCTGGCAG 780
Qy 378 aISerLeuAaPaRGlyAaPheTyRPhaPheLyvGly 391
Db 781 TGTCAATGACTGATGAGATTTCTACTTCTTCAAGGGGT 821
RESULT 4
BM009001 911 bp mRNA linear EST 30-OCT-2001
LOCUS 603618834P1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:542808 5',
DEFINITION mRNA sequence.
ACCESSION BM009001
VERSION BM009001.1 GI:16523355
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 911)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgarbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1881 row: d column: 09
High quality sequence scop: 767.
FEATURES
source location/Qualifiers
1. 911
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:542808"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH_MGC_39"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies)."

ALIGNMENT SCORES:
Pred. No.: 1.19e-97 Length: 911
Score: 1386.50 Matches: 281
Percent Similarity: 92.53% Conservative: 4
Best Local Similarity: 91.23% Mismatches: 12
Query Match: 48.92% Indels: 12
DB: 4 Gaps: 3
US-10-791-980-6 (1-520) x BM009001 (1-911)
Qy 109 LeupheAaPaRGlyAaPheTyRPhaPheLyvGlyAaPaRGInGlyA 128

Db 3 TGTGTTGCTAGACACCGGACCAAGATAGGCGGTGAAGAACGCTTTGGAAAGCAAGTA 62
Qy 128 nLeuTyTlIePheLyvGlySerThIaPheTrpGlyVaIaIaAaSPaRGlyVaSPaRG 147
Db 63 ACAGATGGTACAGAGACGACCTTCCTACCGCTGTGAATGAGCTGAGCACTTGGCCG 122
Qy 148 SerArGInPheGlyVaIaProCySaIaProProSerSerCyvGlyVaIaThSerGInaRG 167
Db 123 AGCCGCGAGTTGGGGCGCGCGGCGGCGCTTCAGATTGGAGCAAGCTCAGCGC 182
Qy 168 TrpSerSerGlyVaRGProGInaPheVaIaPheLeuThrSerGlySerProSerSerLyS 187
Db 183 TGAAGTTTGGAGAGGCGCCAGCAGCAGCGCCGCTGAATCGGCTCACTTCTTCAAG 242
Qy 188 G1YThTrhThrThMeG1YTrPaLaMePProLeuMeTaIaGInGlyVaIaProTrPaRGTrh 207
Db 243 GGGACCAACAAGATGAGGCTGGCAATGCTTGAATGGCCAGAGGAGCGGCTGTGACAG 302
Qy 208 ProPheLeuProArGArGlyGlyVaIaIaIaSPheAaRGInaSPaRGlyVaRGTrpSerLeuSer 227
Db 303 CCTTC-CTGGCCCGCGCGGCGGAGACGACTTCGACCAAGATGAGCGGCTGGTCCCTGAGC 361
Qy 228 ArGaTGAaRGlyAaRGaSPaSPaPheVaIaLeuAaIaIaIaGInSerLeuTyRlyS-ProLe 247
Db 362 CGCCGCGCGCGGCGCAACCTGTTCTGGTGGCGCAGAGATCGTCAACAGCGCTTGGC 421
Qy 248 LeuThrHIsaSPaRGlaProArGlaLeuMeTaIaProTyRlyTyRlyAaPheGlyVaRG 267
Db 422 CTCACCACTGCGCGCGCGCGCGCGCTGACAGGCGCTTACAGAGAGGCTGGAGCGCC 481
Qy 268 AaPaLaLeuLeuSerTrPaSPaSPaPheVaIaLeuAaIaIaGInSerLeuTyRlyS-ProLe 287
Db 482 GACGCGCTGCTAGCTGGGAGAGACGTCGCGCGTGAAGAGCTGTATGGAGAGCCCT 541
Qy 287 nGlyGlySerVaIaIaVaIaGInLeuProGlyLyLeuPheThraPheGlyThTrPaS 307
Db 542 AGGGGCTCAGTGGCGCGCTCCAGCTCCAGAAAGCTGTCACTTGAGAGCTGGGA 601
Qy 307 nSerTySerProGInGlyAaRGaRGProGInThrGInGlyProLyvTyCyvHIsSerSe 327
Db 602 CTCCTACAGCCCCCAAGAGAGCGGCTGAAGCGAAGGCGCTAAATCTGCACTTC 661
Qy 327 rPheAaPaLaIeThTrVaIaAaPaRGInGIn-LeuTyTlIePheLyvGlySerThIaP 347
Db 662 CTTCATGCGCATCAGTGAAGAGGCAAGCAAGCACTTGTACTTTTACCGGAGCAAT 721
Qy 347 nETrGlyVaIaIaAaSPaRGlyAaSPaRGlyVaIaIaAaSPaRGlyVaIaIaAaSPaRG 366
Db 722 TCTGGAGAGTGGCAGCTGATGCAAGCTCAGAGCCCGCTCACTGACAGAAAGAGC 781
Qy 366 pValLyI--LeuProProAaInIeGlyAaIaAaIaVaIaSerLeuAa--AaRG 383
Db 782 GGTGGGAGCTGCGCCCAAAATGAGAGCTTGGGAGAGATGATATGGACAGTCACTGG 841
Qy 383 yAaPheTyRPhaPhePheLyvGlyAaRGySTrPaRGPhaRGlyProLyvProVaI 403
Db 842 CGAATTCATCTTCTTCAAGGGGGGTCAATGCTGAAGTTCCGGGCGCCCAAGCAAGTGT 901
Qy 403 TrpGlyLeu 405
Db 902 GGGGTCTC 909
RESULT 5
BX329088/c 962 bp mRNA linear EST 07-APR-2004
LOCUS BX329088 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS001075YG06 3-PRIME, mRNA sequence.
ACCESSION BX329088
VERSION BX329088.2 GI:46269851
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.
1 (baes 1 to 962)
Li, W. B., Gubler, C., Jesses, J. and Polayes, D.
Full-length cDNA libraries and normalization
On May 2, 2003 14:00:00

FEATURES	source
Location/Qualifiers	1. .962

ORIGIN

Alignment Scores:

Score:	4.63e-93
Percent Similarity:	1328.00
Best Local Similarity:	88.04%
Query Match:	84.36%
8B:	46.86%
	5
	10
	21
	Indels:
	19
	10
	275
	Matches:
	962
	Length:
	4.63e-93

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 /clone="CS0D1075YG06"
 /clone_type="PLACENTA COT 25-NORMALIZED"
 /note="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="First strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 1.19e-80 Length: 1010
 Score: 1169.00 Matches: 264
 Percent Similarity: 81.12% Conservative: 11
 Best Local Similarity: 77.88% Mismatches: 49
 Query Match: 41.25% Indels: 18
 DB: 5 Gaps: 3

US-10-791-980-6 (1-520) x BX349007 (1-1010)

QY 136 SerTyrArgLeuValAsnTrpProGluHisLeu-ArgSerArgGlnPheGlyAlaProCys 155
 DB 3 TCTTACCGCTGTGTAAGTGGCTGAGCATCTGCCGAGCCGCGAGTTCGGGGCCGCTG 62
 QY 155 GAlaProProSerSerCysGlyAlaThrSerGlnArgTrpSerSerGlyArgProGlnPr 175
 DB 63 CGCGCGCTTCACTGTGTGGAGCAACGCTCAGCGCTGGAATTCGGAGGCCCGCAGCC 122
 QY 175 GGlAlaProLeuThrSerGlySerProSerSerGlyThrThrThrMetGlyTrpAl 195
 DB 123 ACAGGCCCCGCGAGCATCGGCTCAGCTTCTCCAGAGGAGACACACATCGGCTGGGC 182
 QY 195 AMePProLeuMetAlaGlnGlyAlaProTrpArgThrPheLeuProArgArgGlyGly 215
 DB 183 AATGCTCTTGATGGCCCGAGGGGGCGGCTGGCGACGCTTC-CTGCCCGCGCGGCGCA 241
 QY 215 uAlaHisPheAspGlnAspGlyArgTrpSerLeuSerArgArgGlyArgAsnLeuPh 235
 DB 242 AGCGCACTTCGACCAAGATGAGCGCTGGTCCCTGAGCGCGCGCGGGCGCACTGTT 301
 QY 235 eValValLeuAlaHisGluHisGlyHisThrLeuGlyLeuThrHisSerProAlaProAr 255
 DB 302 CGTGCTGCTGGCGCAGAGATGGGTCAACGCTTGCCCTCACCTGCCCGCGCGCGCG 361
 QY 255 GAlaLeuMetAlaProTyrTrpLysArgLeuGlyValArgAspAlaLeuLeuSerTrpAspAs 275
 DB 362 CGCGCTCATGGCGCCCTACTACAGAGGCTGGGCGCGACGCGCTGCTGAGCTGGAGCA 421
 QY 275 PValLeuAlaValGlnSerLeuTyrGlyLysProLeuGlyGlySerValAlaValGlnLe 295
 DB 422 CGTGCTGGCGCGAGAGCTGTATGGAGGCCCTTAAAGGGGCTCAGTGGCGCTCAGGC 481
 QY 295 uProGlyLysLeuPheThrAspPheGluThrTrpAspSerTyrSerProGlnGlyArgAr 315
 DB 482 TCCAGAGAAAGCTGTCTACACTCTTGAGACTCTGACCTCTACAGCCCCCAAGAGAGGGG 541
 QY 315 GProGluThrGln-GlyProLysTyrCys-HisSerSer-PheAspAlaHisThrValAs 334
 DB 542 CCTTAAGAGCGAGGGGCGCTTAATAGTCCCACTCTCTCCCTGAGAGGCCATCTGTGA 601
 QY 334 P-ArgGlnGlnGln-LeuTyrHisPhe-LysGlySerHisPheTrp-GluValAlaAla- 352
 DB 602 ACAGGCAACAGCAACTGTCCATTTTAAAGGGAGGCCATTTCTGGGGAGGGGGAGCGC 661
 QY 353 AspGlyAsn---ValSerGluProArgProLeuGlnGluArgTrpVal-GlyLeuProPr 371
 DB 662 GATGCAACCTTCTTAAGAGACCCCGTCCCTGCAAGAAATGGGTGCGMCGCTCCGCC 721
 QY 371 GAsnHisGluAla---AlaAlaValSerLeuAsnAspGlyAspPheTyrPhePhe---Ly 389
 DB 722 CAAATTTGAGGCTTGGGCGAGGCGATCTTGAAGAGAGGAAATCTCTACTTTTCAAAA 781
 QY 389 GglGlyArgCys-TrpArgPheArgGlyProLysProValTrpGlyLeu-ProGlnLeu 408

DB 782 GAGGGGTGATGCTTGGAGAGTCCGGGGCCCCCANACCAAGGGGGGGGTCTTCACAAATTG 841
 QY 409 CysArgAlaGlyGlyLeuProArgHisProAspAlaAlaLeuPheProProLeuArg 428
 DB 842 GTCCCGGAGGGGGCGCTCCCGCCCATCTTA-CCGCGCTTTTCTCTTTTGGC 900
 QY 429 ArgLeuIleLeuPheLysGlyAlaArgTyrTrpValLeuAlaArgGlyGlyLeuGlnVal 448
 DB 901 GCGCTAT-ATCTTTAAGGGTGGCGCTTCAATTAATGTGCGCCGGGGGACTGTATAGC 958
 QY 449 GluProTyrTrpProArgSerLeuGlnAspTrp 459
 DB 959 GCGCCCTTATCCCAATCTTGAAGAGAGTGG 991

RESULT 7

LOCUS BMS44516 1086 bp mRNA linear EST 20-FEB-2002
 DEFINITION AGENCOURT_6491854 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5728282
 5', mRNA sequence.

ACCESSION BMS44516
 VERSION BMS44516.1 GI:18775843
 KEYWORDS EST.

SOURCE
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS NIH-MGC http://mgi.mcl.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bcr-remail.nih.gov
 Tissue Procurement: Invitrogen

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMIL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 . Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILMIL at:
 http://image.llnl.gov
 Plate: LLM12723 row: 1 column: 11
 High quality sequence start: 29
 High quality sequence stop: 685.
 Location/Qualifiers

FEATURES

source

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5728282"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_124"
 /note="Organ: Brain; Vector: pCMV-SPORT6; Site: 1: EcoRV
 (destroyed); Site: 2: NotI; RNA source male hippocampus,
 age 27. Library is oligo-dT primed and directionally
 cloned (EcoRV site is destroyed upon cloning). Average
 insert size 1.4 kb, insert size range 0.9-4 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 012."

ORIGIN

Alignment Scores:

Pred. No.: 2.24e-74 Length: 1086
 Score: 1089.00 Matches: 231
 Percent Similarity: 84.81% Conservative: 9
 Best Local Similarity: 81.63% Mismatches: 23
 Query Match: 38.43% Indels: 20
 DB: 4 Gaps: 6

US-10-791-980-6 (1-520) x BMS44516 (1-1086)

QY 1 MetValAlaArgValGlyLeuLeuLeuArgAlaLeuGlnLeuLeuTrpGlyHisLeu 20

TITLE
JOURNAL
COMMENT

Human ORFeome Version 1.1: a Platform for Reverse Proteomics
Genome Res. (2004) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
results from a PCR reaction using an MGC full-length cDNA as
template DNA and ORF specific primers
PCR Primers
FORWARD: ATGGCGCGCGCGCTGCGCT
BACKWARD: CAACGAGATTCACCTTTGAGA
Insert length: 619 Std Error: 39.00
Plate: 11060 row: 12 column: A
Seq primer: ACTGGCGTGTTCACAGCTGTGACTGGGAAAC
High quality sequence start: 98
High quality sequence stop: 618
POLYA=NO.

FEATURES
source
Location/Qualifiers

1..619
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/feature_type="mixed"
/clone_lib="Full Length cDNA from the Mammalian Gene
Collection"
/note="vector: mixed. The ORFs were PCR amplified from the
MGC (Mammalian Gene Collection) as of April 2004 and
cloned by recombinational Gateway cloning into pDONR223
donor vector. Reference: MGC (Mammalian Gene Collection)
Program Team, Generation and Initial Analysis of more than
15,000 Full-length Human and Mouse cDNA Sequences. PNAS,
2002, 99(26), 16899-16903"

ALIGNMENT SCORES:

Score: 6.23e-70 Length: 619
Percent Similarity: 1027.50 Matches: 200
Best Local Similarity: 97.09% Conservative: 0
Query Match: 36.26% Mismatches: 4
Dbs: 7 Gaps: 3

US-10-791-980-6 (1-520) x CV026222 (1-619)

Qy 1 MetValAlaArgValGlyLeuLeuLeuArgAlaLeuGlnLeuLeuLeuTrpGlyHisLeu 20
Db 1 ATGTGTCGCGCGCTGCGCTCTCTGCGCGCTTCCAGCTCTACTGTGGGCGCACTG 60
Qy 21 AspAlaGlnProAlaGluArgGlyGlyGlnGlnLeuArgGlyGlnAlaGlnAlaPheLeu 40
Db 61 GACGCCGACCGCGCGAGCGCGAGCGCAGAGCTGCGCGAGCGAGCGAGCGAGCTTCTTA 120
Qy 41 GlnuetyrGlyTyrLeuLeuGlnGlnValProlyAlaProThrSerThrArgPheSer 60
Db 121 GAGAAATACGATATCTCAATGAACAGGTCCCAAGCTCCCACTCCATCCATTCAC 180
Qy 61 AspAlaIleArgAlaPheGlnTrpValSerGlnLeuProValSerGlyValLeuAspArg 80
Db 181 GATGCATACAGAGCGCTTCAGTGGGTGTCCAGCTACTCTGACGGCGGTGTGACCGC 240
Qy 81 AlaThrLeuArgGlnMetThrArgProArgCysGlyValThrAspThrAsnSerTyrAla 100
Db 241 GCCACCTTCGCGCAGATGACCTGCGCTGCGGCTTACAGATACCAACAGTTATCG 300
Qy 101 AlaTrpAlaGluArgIleSerAspLeuPheAlaArgHisArgThrIleMetArgArgIys 120
Db 301 GCGTGGGCTGAGGATCACTGATCTGTTCCTAGACACCGGACCAAAATAGCGCGTTAG 360
Qy 121 LysArgPheAlaLysGlnGlnValenlystrTyrIlySGlnHisLeuSerTyrArgLeuVal 140

Db 223 ATGTGTCGCGCGCTGCGCTCTCTGCGCGCTTCCAGCTCTACTGTGGGCGCACTG 282
Qy 21 AspAlaGlnProAlaGluArgGlyGlyGlnGlnLeuArgGlyGlnAlaGlnAlaPheLeu 40
Db 283 GACGCCGACCGCGCGAGCGCGAGCGCAGAGCTGCGCGAGCGAGCGAGCGAGCATTTCTTA 342
Qy 41 GlnuetyrGlyTyrLeuLeuGlnGlnValProlyAlaProThrSerThrArgPheSer 60
Db 343 GAGAAATACGATATCTCAATGAACAGGTCCCAAGCTCCCACTCCATCCATTCAC 402
Qy 61 AspAlaIleArgAlaPheGlnTrpValSerGlnLeuProValSerGlyValLeuAspArg 80
Db 403 GATGCATACAGAGCGCTTCAGTGGGTGTCCAGCTACTCTGACGGCGGTGTGACCGC 462
Qy 81 AlaThrLeuArgGlnMetThrArgProArgCysGlyValThrAspThrAsnSerTyrAla 100
Db 463 GCCACCTTCGCGCAGATGACCTGCGCTGCGGCTTACAGATACCAACAGTTATCG 522
Qy 101 AlaTrpAlaGluArgIleSerAspLeuPheAlaArgHisArgThrIleMetArgArgIys 120
Db 523 GCGTGGGCTGAGGATCACTGATCTGTTCCTAGACACCGGACCAAAATAGCGCGTTAG 582
Qy 121 LysArgPheAlaLysGlnGlnValenlystrTyrIlySGlnHisLeuSerTyrArgLeuVal 140
Db 583 AAACCTTTGCAAGCAAGGTAAACAAATGGTACACACACACTCTCTCCACCGCTGGTG 642
Qy 141 AenTrpProGlnHisLeuArgSerArgGlnPheGlyAlaProCysAlaProPheSer 160
Db 643 AACTGCGCTGAGCATCTGCGCGAGCGCGAGCTTGGGGCGCGTGGCGCGCTTCAG 702
Qy 160 TCGGlyAlaThrSerGlnArgTrpSerSerGlyArgProGlnProGlnAlaProLeuHis 180
Db 703 TTGGAGGCAACGCTTCAGCGCTGAGTGTTCGAGAGCGGCCCAAGCGCCCGCTGAC 762
Qy 180 rSerGlySerProSerSerIysGlyThrThrMetGlyTrpAlaMetProLeuMet 200
Db 763 ATCGGCTACCTCTTCCAGGGGAGACACAGATGGCGCTGGGCAATGCTTGTGATG 822
Qy 200 Ia---GlnGlyAlaProTrpArgThrProPhe---LeuProArgArgGlyGlnAlaHis 217
Db 823 GCCCGAGGGGCGCGCTGCGCGACCCCTTCTCTGCGCGCGCGCGAGCGCACT 882
Qy 218 PheArgGlnAsp---GlnArgTrpSerLeuSerArgArgArgGlyArgAsnLeuPheV 236
Db 883 TTCGACCAAAAGATACACCGCTGTCTCCCTGAGCGCGCGCGCGCGCAAACTG--- 938
Qy 236 aValLeuAlaHisGlnIleGlyHisThr-----LeuGlyLeuThr- 249
Db 939 -----GTTTCTGGGGCGCTGCGCCACACAAATCCGCTCCACCGCTTGGGCTTACCC 993
Qy 250 HisSerPro-----AlaProArgAlaLeuMetAlaProTyrTyrIlyAspArgLeuGly 266
Db 994 AATTCGCCCCGGGGGGGGGGGCTCATGACGCGCTTACTTAACAAAAGCTGGG 1050

RESULT 8
CV026222
LOCUS
DEFINITION
4093 full length cDNA from the Mammalian Gene Collection Homo
Accession
CV026222
VERSION
CV026222.1 GI:51484195
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RuiJ.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S.,
Dietz, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O.,
Clintonsmith, T.R., Hartley, J.L., Espósito, D., Cheo, D., Moore, T.,
Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C.,
Vandenhaute, J., Cusick, M.E., Albaladejo, J.S., Hill, D.E. and Vidal, M.

Db 361 AACCCCTTGGCAACCAAGGTACAAATGGTACAGCAGCACTCTCCACCGCTGGTG 420
 Qy 141 AentrpProgluHisIeu-ArgSerArgInpHeIyIaProCyAlaProProSe 160
 Db 421 AACTGGCCCTGAGCATTCTGGGAGCGGAGTTCGGGGCGCTGCGGCCCTTCCAG 480
 Qy 160 rCyegIyAlaThrsSerGlnArgTrpSerSerGlyArgProGlnProGlnAlaProLeuTh 180
 Db 481 TTGTGAGCAACAGTCTCAGCGCTGAGATTCTGGAGGCCCCAGCCACAGGCCCGCTGAC 540
 Qy 180 rSerGlySerProSerSerGlyGlyThrThrThrMetGlyTrpAlaMetProLeuMetAl 200
 Db 541 ATCCGGCTCACCTTCTTCCAAAGGAGCACAAGATGGGCTGGGC-ATGCCCTTATAGCC 599
 Qy 200 aGlnGlyAlaProTrp 205
 Db 600 CANGGCG---CCCTGG 612

RESULT 9
 B0694961
 LOCUS 1001104 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens
 DEFINITION B0694961 587 bp mRNA linear EST 15-JUL-2002
 CDNA 5', mRNA sequence.
 ACCESSION B0694961
 VERSION B0694961.1 GI:21820277
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 587)
 AUTHORS Yang, R.-Z., Shuldiner, A. and Gong, D.-W.
 TITLE EST analysis of human adipose gene expression
 JOURNAL Unpublished (2002)
 COMMENT Contact: Gong Da-Wei
 Division of Endocrinology, Diabetes and Nutrition
 University of Maryland
 660 Redwood St., HH497, Baltimore, MD 21201, USA
 Tel: 410 706 1672
 Fax: 410 706 1622
 Email: dgong@medicine.umaryland.edu
 PCR PRIMERS
 FORWARD: CTCGGGAGCGCGCATGTGTGTGT
 BACKWARD: AATACGACTCCTATAGGCGGAATTGG
 Seq primer: CTGGCTACCGCGGAATTC.
 FEATURES
 source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /sex="Male and Female"
 /tissue_type="Adipose"
 /clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
 /note="Vector: lambdaTriplex"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,226-68 Length: 587
 Score: 1010.50 Matches: 192
 Percent Similarity: 98.47% Conservative: 1
 Best Local Similarity: 97.96% Mismatches: 3
 Query Match: 35.66% Indels: 2
 DB: 5 Gaps: 0

US-10-791-980-6 (1-520) x B0694961 (1-587)
 Qy 211 ProaGATGAGlyGlyAlaHisPheAapGlnAapGluArgTrpSerLeuSerArgArg 230
 Db 1 CCCGCCCGCGGAGGAGCGCATTCACACAAATGAGCGCTGTCCTTAGCGCGCGCGC 60
 Qy 231 GlyArgAenLeuPheValIleuAlaHisGluIleGlyHisThrLeuGlyLeuThHis 250

Db 61 GGGCGCAACCTGTTGCTGCTGCGCGCAGAGATCGGTCAACGCTTGCCACCCAC 120
 Qy 251 SerProAlaProaGAlaLeuMetAlaProTyTrpYIySaArgLeuGlyArgAapAlaLeu 270
 Db 121 TCGCCCGCGCGCGCGCGCTCATGGCGCCCTACATCAAGAGAGCTGGGCGGAGCGGCTG 180
 Qy 271 LeuSerTrpAapAapValIleuAlaValGlnSerLeuTyGlyIyVProLeuGlyGlySer 290
 Db 181 CTGAGCTGGAGACAGCTGCTGGCGCGTGCAGAGCCGTATGGGAAGCCCCCTAGGGGGCTCA 240
 Qy 291 ValAlaValGlnLeuProGlyIyIyLeuPheThrAapPheGluThrTrpAapSerTySer 310
 Db 241 GTGGCGGTCCAGCTCCAGAAAGCTGTCACTGTGAGACCTTGAGACTTGACCTTACAGC 300
 Qy 311 ProGlnGlyArgArgProGluThrGlnGlyProIyTyTyCyHisSerSerPheAapAla 330
 Db 301 CCCAAGAGAGGCGCGCTGAAACGAGGCGCCCTAAATCTGCCACTCTTCTGTGATGCC 360
 Qy 331 IleThrValAapArgGlnGlnLeuTyTrpIlePheGlySerHisPheTrpGluVal 350
 Db 361 ATCACTGTAGACAGGACACAGCACTGTACATTTTAAAGGAGGCCATTTCTGGGAGGCTG 420
 Qy 351 AlaAlaAapGlyAenValSerGluProArgProLeuGlnGluArgTrpValGlyLeuPro 370
 Db 421 GCAGCTGATGGCAACGTCTCAGAGCGCGTCCACTGCAGAAAGATGGGTGGGCTGCC 480
 Qy 371 ProaenIleGluAlaAlaValSerLeuAenAapGlyAapPheTyPhePheGlyGly 390
 Db 481 CCAC-ATTGAGGCTGCGCGAGCTGATGATGATGAGATTTTACTTCTTCAAAGGG 539
 Qy 391 GlyArgCyTrpArgPheArgGlyProIyAProValTrpGlyLeuPro 406
 Db 540 GGTGATCTCTGAGAGGTTGG--GGGCCCAACAGAGTGGGGGTCTCCCA 585

RESULT 10
 BMS60236
 LOCUS 1065 bp mRNA linear EST 20-FEB-2002
 DEFINITION AGENCOURT 6564030 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5744676
 5', mRNA sequence.
 ACCESSION BMS60236
 VERSION BMS60236.1 GI:18804497
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1065)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgs@bbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/MLN at:
 http://image.llnl.gov
 Plate: LLM12766 row: 9 column: 13
 High quality sequence stop: 660.
 FEATURES
 source
 1..1065
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5744676"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_119"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and

Oy		455	SerLeuGlnAagTTrgIAGlylleProGuGUValSeRGlyAlaLeuProArgProAsp	474
Dd		335	AGTTTGCAAGACTGGGAGGCATCTCCTTAGAGAGGTACAGCGGCCCTTCGCAAGGCCCAT	276
Oy		475	GlySerllelePhePheArgAspaAspaArgTyrrTPatGLeuAspGlnAlaLysLeuGln	494
Dd		275	GGCTCCATCATCTTTTTTCGAGATGACCGCTACTGGCGCTCTGCACAAGCCAAACTGGAC	216
Oy		495	AlAtTrThrSerGlyVAgtTPAlaThrGluLeuPcOTrPMetGlyCyatTPHisAlaAsn	514
Dd		215	GCAACACCACCTCGGGCGCGCTGGCCACACGAGCTGCCCTGGATGGCTGTGGCATCCCAAC	156
Oy		515	SerglSerAlalaLeuPhe	520
Dd		155	TGGGGAGCGCCCTGTATT	138
RESULT 12				
LOCUS	BX280995		499 bp	mRNA linear EST 04-MAR-2003
DEFINITION	BX280995 NIH_MGC_121 Homo sapiens cDNA clone IMAGE99800411626 ;			
ACCESSION	IMAGE:5248347, mRNA sequence.			
VERSION	BX280995			
KEYWORDS	BX280995.1 GI:28612561			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
TITLE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
COMMENT	1 (bases 1 to 499) Ebert,L., Hell,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B. Human Unigeneset - RZPD Unpublished (2003) Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD, IMAGP99800411626. RZPDLIB, I.M.A.G.E. cDNA Clone Collection; Human Unigeneset - RZPD (RZPDLIB No.972) http://www.rzpd.de/ClsoneCards/cgi- bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: Mish, Primer sequence: CGTGTAAAAGACGGCCAGT. Location/Qualifiers 1..499 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGP99800411626 ; IMAGE:5248347" /lab_host="DH10B" /clone_lib="NIH_MGC_121" /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."			
ORIGIN				
Alignment Scores:				
Pred. No.:	1,01e-57	Length:	499	
Score:	869.00	Matches:	165	
Percent Similarity:	98.80%	Conservative:	0	

Best Local Similarity:	98.80%	Mismatches:	1
Query Match:	30.66%	Indels:	2
DB:	5	Gaps:	0
US-10-791-980-6 (1-520) x BX280995 (1-499)			
QY	119	ArglyblybAaRphEAlaIyEgLIgLYaNslybTPrLYbGNIaIeUsEryArG	138
DB	2	CGTAAAGAAACCTTTGCAAGAGAGATGAACAAATGGTACAGACACCTCTCTACGGC	61
QY	139	LeuValaantPrProGluNIaIeU-ArgSerArgGInPheGlyAlaProCybAlaProPr	158
DB	62	CTGGGAAACTGGCCCGAGACATCTGCGGAGCGGAGATTGGGGGGCGCGTGGCGCGCC	121
QY	158	oSerSerCyGlyAlaIathrSerGInaYTrpSerSerGlyAlaPrProGInPProGInAlaPr	178
DB	122	TTCCAGTTGTGGAGCAACGCTCAGCGCTGGAGTTCTGGAGAGCCCCAGCACAAGGCCCC	181
QY	178	oleUthSerIySerProSerSerIyGlyIthThrThaMetGlyTPrAlaMetProIe	198
DB	182	GCTGACATCCGACCTCACCTTCTTCCAAAGGAGACCAACAGATGGGCTGGCAATGCCCTTT	241
QY	198	uMeAlaGInGlyAlaProTPrArGthProPheUeProArGArGlyGlyAlaNIaIePh	218
DB	242	GATGGCCCGAGGGGGCGCCCTGGCGCACGCCCTTC-CTGCCCGCGCGCGGAGGCCACTT	300
QY	218	eASpGInaPpGlyAlaYTrpSerLeuSerArgArGArGlyAlaIrgaNIeUaPheValIe	238
DB	301	CGACCAAGATAGCGCTGTCCCTGAGCGCGCGCGGCGCAACCTGTTCTGTGTCTT	360
QY	238	uAlaIaGluIleGlyAlaIsthTrIeUglyIleuThrHisEserProAlaProAlaGlyAlaUe	258
DB	361	GGCCGACAGATCGGTCAACAGCTTGGCTCACCCACACCGCGCGCGCGCTCAT	420
QY	258	fAlaProTPrYrlybAaRphEAlaIyEgLIyArGAspAlaIeUeUsErtPrAsPavAlIeUaI	278
DB	421	GGCGCCCTACTACAGAGGCTGGGCGCGACGCGCTCTCAGCTGGAGCAGACTCTGGC	480
QY	278	aValGInSerLeuTyrgly 284	
DB	481	CGTGAGAGCGCTGTATGGG 499	
RESULT 13			
LOCUS	BX360790	958 bp	linear EST 08-APR-2004
DEFINITION	BX360790 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA		
ACCESSION	BX360790	GI:46306660	
VERSION	BX360790.2	GI:46306660	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 958)		
JOURNAL	L.I.W.B., Gruber,C., Jeesee,J. and Polayes,D.		
COMMENT	Full-length cDNA libraries and normalization		
	Unpublished (2001)		
	On May 5, 2003 this sequence version replaced gi:30378467.		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE		
	Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr		
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers		
	end enriched, double-strand cDNA was digested with Not I and cloned		
	into the Not I and BclII sites of the pCMVSPORT 6 vector. Library		
	was normalized. Library was constructed by Life Technologies, a		
	division of Invitrogen. This sequence belongs to sequence cluster		
	8754.r		
	For more information about this cluster, see		
	http://www.genoscope.cns.fr/cdna?b=CS001075BD03QPl&c=8754.r.		
FEATURES	Location/Qualifiers		
SOURCE	1..958		

ORIGIN

Alignment Scores:

Pred. No.: 1,57e-55
Score: 846.00
Percent Similarity: 90.50%
Best Local Similarity: 89.14%
Query Match: 29.85%
DB: 5

US-10-791-980-6 (1-520) x BX360790 (1-958)

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS01075XG06"
/issue_type="PLACENTA"
/note="Homo sapiens PLACENTA COT 25-NORMALIZED"
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

Length: 958
Matches: 197
Conservative: 3
Mismatch: 15
Indels: 13
Gaps: 4

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QY      1 MetValAlaArgValGlyLeuLeuLeuAArgAlaLeuGlnLeuLeuTrpGlyHisLeu 20
Db      248 ATGGTCCGCGCGCGCTCCCTGCTGCGCGCGCTGCAAGCTGCTGAGGCGCACTG 307
QY      21 AspAlaGlnProAlaGlnArgGlyGlnGlnLeuArgGlyGlnAlaGlnAlaPheLeu 40
Db      308 GAGGCCACCGCCGCGAGGCTGA-GCCAGAGAGCTGCGCAAGAGCGGAGGATTCCTTA 366
QY      41 GlnLeuTrpGlyLeuLeuGlnGlnValProLeuAlaProThrSerThrArgPheSer 60
Db      367 GAGAAGTACGATACCTCAATGAACAGGATCCCAAACTCCCACTCCATCGATTACAC 426
QY      61 AspAlaIleArgAlaPheGlnTrpValSerGlnLeuProAlaSerGlyValLeuAspArg 80
Db      427 GATGCGCATCAGAGCGCTTCACTGGGTCTCCAGCTTACCTGCGCGCTGTGGACCGC 486
QY      81 AlaThrLeuArgGlnMetThrArgProArgCysGlyValThrAspThrAsnSerTyrAla 100
Db      487 GCCACCCCTGCGCCAGATGACTCGTCCCGCTGCGGGGTTACAGATACCAACGTTATGCG 546
QY      101 AlaTrpAlaGlnArgIleSerAspLeuPheAlaArgHisArgThrLeuMetArgArgLys 120
Db      547 GCGTGGGCTGAGAGATCACTGACTTGTCTTACACCGGACCAAAATAGAGCGCTAAG 606
QY      121 LysArgPheAlaLeuGlnGlnGlnValSerTyrLeuGlnHisLeuSerTyrArgLeuVal 140
Db      607 AAACGCTTTCAGAAAGAGTAAACAATGTACAAAGCAGACCTCTCTACCGCTGTG 666
QY      141 AsnTrpProGlnHisLeu-ArgSerArgGlnPheGlyValaProCysAlaProProSerSe 160
Db      667 AACTGGCTGACACATCTGCGGAGCGGCGAGTTCGGGGCGCGGTGCGG-CGGCTTCCAG 725
QY      160 TCysGlyAlaThrSerGlnArgTrpSerSerGlyArgProGlnProGlnAlaProLeuHis 180
Db      726 TTGTGGAGC-ACGTCTCAGCCCTGAGTTCGGGAGGCGCCAG-CCACAGGC-CCGCTGAC 782
QY      180 rSerGlySerProSerSerLeuGlyThrThrThrMetGlyTrpAlaMetProLeuMetAl 200
Db      783 ATCTGCTC-ACCTCTTCMAAGGAGACACAGATGCTGGGCTGCT-----TTATATGCG 834
QY      200 aGlnGlyAlaIleProTrpArgThrProPheLeuProArgArgGlyGlnAlaHisPheAspG 220
Db      835 CAGGCGCGCGC---TGC---CSAGCTTCTGCGCG--CGSGGAGAG---CACTTTCACCA 883
QY      220 n 220
Db      884 G 884

```

RESULT 14
BP325923
LOCUS

BP325923 581 bp mRNA linear EST 17-SEP-2004

DEFINITION

BP325923 Sugano cDNA library, prostate Homo sapiens cDNA clone

PS000515, mRNA sequence.

ACCESSION

BP325923

VERSION

BP325923.1

KEYWORDS

EST, 512254909

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 581)

AUTHORS

Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,

TITLE

Sequence comparison of human and mouse genes reveals a homologous

JOURNAL

block structure in the promoter regions

COMMENT

Genome Res. 14 (9), 1711-1718 (2004)

CONTACT

Department of Virology

INSTITUTE

Institute of Medical Science, University of Tokyo

ADDRESS

4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan

E-MAIL

Email: yasukie@ims.u-tokyo.ac.jp.

FEATURES

source

1..581

location/Qualifiers

1..581

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="PS000515"

/issue_type="prostate"

/clone_lib="Sugano cDNA library, prostate"

ORIGIN

Alignment Scores:

Pred. No.: 7.29e-55
Score: 833.50
Percent Similarity: 67.94%
Best Local Similarity: 67.94%
Query Match: 29.41%
DB: 5

US-10-791-980-6 (1-520) x BP325923 (1-581)

Length: 581
Matches: 178
Conservative: 0
Mismatch: 7
Indels: 78
Gaps: 1

```

QY      42 LysTrpGlyTyrLeuGlnGlnValaProLeuAlaProThrSerThrArgPheSerAsp 61
Db      3 AAGTACGGATTCCTCATGAAACAGTCCCAAGGCTCCCACTCCATCGATTACGCAT 62
QY      62 AlaIleArgAlaPheGlnTrpValSerGlnLeuProValSerGlyValLeuAspArgAla 81
Db      63 GCATTCAGACCGCTTTCAGTGGGTGTCCTCCAGTACCTGTCAAGCGCGCTTGGACCGGCC 122
QY      82 ThrLeuArgGlnMetThrArgProArgCysGlyValaThrArgThrAsnSerTyrAlaAla 101
Db      123 ACCCTGCGCAGATGACTGCTCCCGCTGCGGGTTACAGATACCAACAGTTATGCCGCC 182
QY      102 TrpAlaGlnArgIleSerAspLeuPheAlaArgHisArgThrLysMetArgArgLysVal 121
Db      183 TTGGCTGAGAGATCAAGTACTGTTGCTAGACCGGACCAAAATAGAGCGCTTAAGAA 242
QY      122 ArgPheAlaLysGlnGlnValaLysLysTrpTyrLysGlnHisLeuSerTyrArgLeuVala 141
Db      243 CCGCTTGGAAAG----- 254
QY      142 TrpProGlnHisLeuArgSerArgGlnPheGlyValaProCysValaProProSerSerCys 161
Db      254 ----- 254
QY      162 GlyAlaThrSerGlnArgTrpSerSerGlyArgProGlnProGlnAlaProLeuThrSer 181
Db      254 ----- 254
QY      182 GlySerProSerSerLysGlyThrThrThrMetGlyTrpAlaMetProLeuMetAlaGln 201
Db      255 -----CAA 257
QY      202 -GlyAlaProTrpArgThrProPheLeuProArgArgGlyValaLysHisPheAspGlna 221

```

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Db      258 GGGGGCGCCCTGCGCCACCCCTTC-CTGCCCCCGCGCGGAGGCGACTTCGACCAAGA 316
Qy      221 PGLuArGTTPSeRLeuSeRArgARgARgLYARgAnLeu-PhyVa1Val1eua1aH1ag 241
Db      317 TGAGCGCTGTGTCCCTGAGCCGCGCGCGGCGCAACCTGTTGCGGAGCTGGGCGACG 376
Qy      241 Lu1leG1YH1eThReuG1YLeuThH1eSeRProh1aPRArGA1aLeuMe1a1aProT 261
Db      377 AGATGGGTCAACGCTTGNCCTACCCCACTCCCGCGCGCGCGGCTCATGGGCGCT 436
Qy      261 YTYTYLYARgLeuG1YARgAPa1aLeuLeuSeRTTPhAPhAP1a1eua1aVa1G1NS 281
Db      437 ACTACAGAGGCTGAGCCGCGCGGCGCTGCTCAGCTMGACGACGCTGCGCGGCGA 496
Qy      281 eRLeuTYrG1YLYARgProLeuG1YSeRVA1a1Va1G1nLeuProG1YLYARgLeuPhet 301
Db      497 GCTGTATAGGAAGCCCTTANGGGGCTTAGTG3CCGCTCCAGCTTCCAGTAAGCTGTCA 556
Qy      301 hr 301
Db      557 CT 558

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RESULT 15
BQ722257      1310 bp mRNA linear EST 16-JUL-2002
LOCUS      BQ722257
DEFINITION  AGENCOURT 8291272 lupsk1 sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6193589 5', mRNA sequence.
ACCESSION  BQ722257
VERSION     BQ722257.1 GI:21861154
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

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REFERENCE
AUTHORS      1 (bases 1 to 1310)
TITLE        NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM13598 row: h column: 22
High quality sequence start: 111
High quality sequence stop: 344.
Location/Qualifiers

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FEATURES

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6193989"
/sex="male"
/cisue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_1lb="lupsk1 sympathetic trunk"
/notes="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGACCCACGCGTCCG-3' and
5'-GACTATGCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

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Alignment Scores:
Pred. No.: 2,166-53 Length: 1310
Score: 821.00 Matches: 154
Percent Similarity: 85.03% Conservative: 5
Best Local Similarity: 82.35% Mismatches: 23
Query Match: 28.97% Indels: 5
DB: 5 Gaps: 1

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US-10-791-980-6 (1-520) x BQ722257 (1-1310)

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Qy      326 SerSeRPhenAPa1a1eThVa1aPaRg1ng1ng1nLeuTYr11ePhelySeR 345
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Qy      346 H1SPheTPG1uVa1a1a1aSPG1YABNValSeRg1uPProARgProLeuG1ng1uArg 365
Db      143 CATTTCTGGAGAGTGGAGCTGATGAGCAAGCTCTAGAGCCCGTCCACTGAGAGAAAGA 202
Qy      366 TPVa1G1YLeuProProABn1leG1u1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a 385
Db      203 TGGGTGGGGCTGCCCCCAATTGAGGCTGGGCGAGTGTATTGAATGATGAGATTTC 262
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Qy      406 ProG1nLeuCYARgA1aG1YLYARgProARgH1SPROABPA1a1a1eUphPhPro 425
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